(54) Title: METHOD FOR DISTINGUISHING WHO CLASSIFIED AML SUBTYPES

(57) Abstract: Disclosed is a method for distinguishing WHO classified AML subtypes AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a, AML_M5b, AML_M6, AML_t(15;17)/M3 and/or AML_t(15;17)/M3v in a sample by determining the expression level of markers, as well as a diagnostic kit and an apparatus containing the markers.

Method for distinguishing WHO classified AML subtypes

The present invention is directed to a method for distinguishing WHO classified AML subtypes, in particular AML subtypes t(15;17); t(8;21); inv(16); 11q23; de novo_AML, AML following MDS (s_AML), therapy-related AML (t_AML); AML_t(15;17)/M3 and AML_t(15;17)/M3v by determining the expression level of selected marker genes.

Leukemias are classified into four different groups or types: acute myeloid (AML), acute lymphatic (ALL), chronic myeloid (CML) and chronic lymphatic leukemia (CLL). Within these groups, several subcategories can be identified further using a panel of standard techniques as described below. These different subcatgories in leukemias are associated with varying clinical outcome and therefore are the basis for different treatment strategies. The importance of highly specific classification may be illustrated in detail further for the AML as a very heterogeneous group of diseases. Effort is aimed at identifying biological entities and to distinguish and classify subgroups of AML which are associated with a favorable, intermediate or unfavorable prognosis, respectively. In 1976, the FAB classification was proposed by the French-American-British co-operative group which was based on cytomorphology and cytochemistry in order to separate AML subgroups according to the morphological appearance of blasts in the blood and bone marrow. In addition, it was recognized that genetic abnormalities occurring in the leukemic blast had a major impact on the morphological picture and even more on the prognosis. So far, the karyotype of the leukemic blasts is the most important independent prognostic factor regarding response to therapy as well as survival.

Usually, a combination of methods is necessary to obtain the most important information in leukemia diagnostics: Analysis of the morphology and cytochemistry of bone marrow blasts and peripheral blood cells is necessary to establish the diagnosis. In some cases the addition of immunophenotyping is mandatory to separate very undifferentiated AML from acute lymphoblastic leukemia and CLL. Leukemia subtypes investigated can be diagnosed by cytomorphology alone, only if an expert reviews the smears. However, a genetic analysis based on chromosome analysis, fluorescence in situ hybridization or RT-PCR and immunophenotyping is required in order to assign all cases in to the right

category. The aim of these techniques besides diagnosis is mainly to determine the prognosis of the leukemia. A major disadvantage of these methods, however, is that viable cells are necessary as the cells for genetic analysis have to divide in vitro in order to obtain metaphases for the analysis. Another problem is the long time of 72 hours from receipt of the material in the laboratory to obtain the result. Furthermore, great experience in preparation of chromosomes and even more in analyzing the karyotypes is required to obtain the correct result in at least 90% of cases. Using these techniques in combination, hematological malignancies in a first approach are separated into chronic myeloid leukemia (CML), chronic lymphatic (CLL), acute lymphoblastic (ALL), and acute myeloid leukemia (AML). Within the latter three disease entities several prognostically relevant subtypes have been established. As a second approach this further sub-classification is based mainly on genetic abnormalities of the leukemic blasts and clearly is associated with different prognoses.

The sub-classification of leukemias becomes increasingly important to guide therapy. The development of new, specific drugs and treatment approaches requires the identification of specific subtypes that may benefit from a distinct therapeutic protocol and, thus, can improve outcome of distinct subsets of leukemia. For example, the new therapeutic drug (STI571) inhibits the CML specific chimeric tyrosine kinase BCR-ABL generated from the genetic defect observed in CML, the BCR-ABL-rearrangement due to the translocation between chromosomes 9 and 22 (t(9;22) (q34; q11)). In patients treated with this new drug, the therapy response is dramatically higher as compared to all other drugs that had been used so far. Another example is the subtype of acute myeloid leukemia AML M3 and its variant M3v both with karyotype t[15;17](q22; q11-12). The introduction of a new drug (all-trans retinoic acid - ATRA) has improved the outcome in this subgroup of patient from about 50% to 85 % long-term survivors. As it is mandatory for these patients suffering from these specific leukemia subtypes to be identified as fast as possible so that the best therapy can be applied, diagnostics today must accomplish sub-classification with maximal precision. Not only for these subtypes but also for several other leukemia subtypes different treatment approaches could improve outcome. Therefore, rapid and precise identification of distinct leukemia subtypes is the future goal for diagnostics.

Thus, the technical problem underlying the present invention was to provide means for leukemia diagnostics which overcome at least some of the disadvantages of the prior art diagnostic methods, in particular encompassing the time-consuming and unreliable combination of different methods and which provides a rapid assay to

5   unambigously distinguish one AML subtype from another, e.g. by genetic analysis.

According to Golub et al. (Science, 1999, 286, 531-7), gene expression profiles can be used for class prediction and discriminating AML from ALL samples. However, for the analysis of acute leukemias the selection of the two different subgroups was

10   performed using exclusively morphologic-phenotypical criteria. This was only descriptive and does not provide deeper insights into the pathogenesis or the underlying biology of the leukemia. The approach reproduces only very basic knowledge of cytomorphology and intends to differentiate classes. The data is not sufficient to predict prognostically relevant cytogenetic aberrations.

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Furthermore, the international application WO-A 03/039443 discloses marker genes the expression levels of which are characteristic for certain leukemia, e.g. AML subtypes and additionally discloses methods for differentiating between the subtype of AML cells by determining the expression profile of the disclosed

20   marker genes. However, WO-A 03/039443 does not provide guidance which set of distinct genes discriminate between two subtypes and, as such, can be routineously taken in order to distinguish one AML subtype from another.

The problem is solved by the present invention, which provides a method for

25   distinguishing WHO classified AML subtypes AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a, AML_M5b, AML_M6, AML_t(15;17)/M3 and/or AML_t(15;17)/M3v in a sample, the method comprising determining the expression level of markers selected from the markers identifiable by their

30   Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, 3, 4, 5, 6 and/or 7,

        wherein

                a lower expression of at least one polynucleotide defined by any of the
                numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20,

21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 1.1

is indicative for the presence of AML_MLL when AML_MLL is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 1.2

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from all other subtypes,

and/or wherein

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 1.3 and/or

a lower expression of at least one polynucleotide defined by any of the numbers 41 of Table 1.3

is indicative for the presence of AML_other when AML_other is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 1.4

is indicative for the presence of AML_t(15;17) when AML_t(15;17) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 1.5

is indicative for the presence of AML_t(8;21) when AML_t(8;21) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 3, 4, 5, 6, 7, 11, 12, 13, 15, 16, 17, 19, 20, 22, 24, 25, 27, 28, 30, 31, 32, 33, 34, 35, 37, 41, 42, 43, 44, 46, 48, and/or 50 of Table 2.1, and or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 8, 9, 10, 14, 18, 21, 23, 26, 29, 36, 38, 39, 40, 45, 47, and/or 49 of Table 2.1,

is indicative for the presence of AML_MLL when AML_MLL is distinguished from AML_inv(16),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 2.2

is indicative for the presence of AML_MLL when AML_MLL is distinguished from AML_other,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 5, 6, 7, 8, 9, 11, 13, 15, 18, 20, 22, 24, 25, 26, 27, 29, 30, 33, 34, 35, 36, 41, 44, 46, , and/or 50 of Table 2.3, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 4, 10, 12, 14, 16, 17, 19, 21, 23, 28, 31, 32, 37, 38, 39, 40, 42, 43, 45, 47, 48, and/or 49 of Table 2.3

is indicative for the presence of AML_MLL when AML_MLL is distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 8, 13, 17, 18, 19, 23, 26, 27, 28, 29, 35, 38, 39, 40, 43, 45, and/or 50 of Table 2.4, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 14, 15, 16, 20, 21, 22, 24, 25, 30, 31, 32, 33, 34, 36, 37, 41, 42, 44, 46, 47, 48, and 49 of Table 2.4,

is indicative for the presence of AML_MLL when AML_MLL is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 2.5, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 37 of Table 2.5

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from AML_other,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 2, 4, 7, 9, 12, 17, 22, 23, 28, 29, 30, 34, 39, 42, and/or 49 of Table 2.6, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 3, 5, 6, 8, 10, 11, 13, 14, 15, 16, 18, 19, 20, 21, 24, 25, 26, 27, 31, 32, 33, 35, 36, 37, 38, 40, 41, 43, 44, 45, 46, 47, 48, and/or 50 of Table 2.6,

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 6, 15, 27, 32, 36, 44, and/or 47, of Table 2.7, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 7, 8, 9, 10, 11, 12, 13, 14, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 28, 29, 30, 31, 33, 34, 35, 37, 38, 39, 40, 41, 42, 43, 45, 46, 48, 49, and/or 50 of Table 2.7,

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 18, and/or 25 of Table 2.8, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 2.8,

is indicative for AML_other when AML_other is distinguished from AML_t(15;17),

and/or wherein

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 2.9,

is indicative for AML_other when AML_other is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 4, 7, 11, 14, 16, 18, 22, 23, 24, 25, 27, 29, 31, 32, 33, 36, 37, 38, 41, 42, 43, 47, 48, and/or 49, of Table 2.10,

a higher expression of at least one polynucleotide defined by any of the numbers 2, 3, 5, 6, 8, 9, 10, 12, 13, 15, 17, 19, 20, 21, 26, 28, 30, 34, 35, 39, 40, 44, 45, 46, and/or 50 of Table 2.10

is indicative for AML_t(15;17) when AML_t(15;17) is distinguished from AML_t(8;21),

and/or wherein

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 3.1,

is indicative for denovo_AML when denovo_AML is distinguished from all other AML subtypes

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 3.2,

is indicative for s_AML when s_AML is distinguished from all other AML subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 3.3,

is indicative for t_AML when t_AML is distinguished from all other AML subtypes

and/or wherein

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 4.1,

is indicative for denovo_AML when denovo_AML is distinguished from s_AML,

and/or wherein

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 4.2,

is indicative for denovo_AML when denovo_AML is distinguished from t_AML

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 7, 8, 12, 13, 15, 16, 17, 19, 21, 22, 23, 24, 25, 30, 31, 34, 35, 36, 37, 38, 41, 45, 47, and/or 50 of Table 4.3, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 9, 10, 11, 14, 18, 20, 26, 27, 28, 29, 32, 33, 39, 40, 42, 43, 44, 46, 48, and/or 49 of Table 4.3,

is indicative for s_AML when s_AML is distinguished from t_AML

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 5.1,

is indicative for AML_M0 when AML_M0 is distinguished from all other AML subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 5.2,

is indicative for AML_M1 when AML_M1 is distinguished from all other AML subtypes

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 33, 34, 35, 36, 37, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 5.3, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 32 and/or 38 of Table 5.3

is indicative for AML_M2 when AML_M2 is distinguished from all other AML subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 19, 20, 21, 22, 25, 26, 27, 29, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 5.4, and/or

a higher expression a polynucleotide defined by any of the numbers 18, 23, 24, 28, and/or 30 of Table 5.4

is indicative for AML_M4 when AML_M4 is distinguished from all other AML subtypes

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 5.5,

is indicative for AML_M5a when AML_M5a is distinguished from all other AML subtypes

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 8, 9, 10, 11, 12, 13, 14, 15, 17, 18, 19, 21, 22, 23, 24, 25, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 39, 40, 42, 43, 44, 46, 48, 49, and/or 50 of Table 5.6, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 6, 7, 16, 20, 26, 37, 38, 41, 45, and/or 47 of Table 5.6,

is indicative for AML_M5b when AML_M5b is distinguished from all other AML subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 5.7,

is indicative for AML_M6 when AML_M6 is distinguished from all other AML subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, and/or 50 of Table 6.1, and/or

a higher expression a polynucleotide defined by any of the numbers 36, and/or 49 of Table 6.1

is indicative for AML_M0 when AML_M0 is distinguished from AML_M1,

5   and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 6.2

10   is indicative for AML_M0 when AML_M0 is distinguished from AML_M2,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 6.3, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 9 of Table 6.3,

is indicative for AML_M0 when AML_M0 is distinguished from AML_M4,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 3, 5, 7, 9, 11, 12, 14, 18, 26, 32, 33, 34, 35, 36, 39, 40, 41, 42, 43, 44, 45, 47, 48, and/or 49, of Table 6.4, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 2, 4, 6, 8, 10, 13, 15, 16, 17, 19, 20, 21, 22, 23, 24, 25, 27, 28, 29, 30, 31, 37, 38, 46, and/or 50 of Table 6.4,

is indicative for AML_M0 when AML_M0 is distinguished from AML_M5a,

30   and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19,

20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 6.5

is indicative for AML_M0 when AML_M0 is distinguished from AML_M5b

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 7, 8, 9, 10, 18, 26, 27, 28, 30, 32, 34, 35, 36, 37, 39, 46, 47, 48, and/or 49, of Table 6.6, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 11, 12, 13, 14, 15, 16, 17, 19, 20, 21, 22, 23, 24, 25, 29, 31, 33, 38, 40, 41, 42, 43, 44, 45, and/or 50 of Table 6.6

is indicative for AML_M0 when AML_M0 is distinguished from AML_M6,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 37, 40, 41, 42, 44, 45, 46, 47, 48, 49, and/or 50 of Table 6.7

a higher expression of at least one polynucleotide defined by any of the numbers 9, 24, 36, 38, 39, and/or 43, of Table 6.7

is indicative for AML_M1 when AML_M1 is distinguished from AML_M2,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 4, 5, 6, 7, 8, 9, 10, 11, 13, 15, 17, 18, 19, 21, 22, 24, 25, 26, 27, 28, 29, 30, 31, 32, 34, 35, 36, 37, 38, 40, 41, 42, 43, 44, 45, 47, 48, 49, and/or 50 of Table 6.8, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 3, 12, 14, 16, 20, 23, 33, 39, and/or 46 of Table 6.8,

is indicative for AML_M1 when AML_M1 is distinguished from AML_M4,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 23, 25, and/or 47, of Table 6.9, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 24, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 48, 49, and/or 50 of Table 6.9,

is indicative for AML_M1 when AML_M1 is distinguished from AML_M5a,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 7, 8, 9, 10, 11, 12, 13, 14, 15, 17, 18, 20, 22, 23, 24, 26, 28, 29, 31, 32, 33, 35, 38, 40, 41, 42, 45, 46, 48, 49, and/or 50 of Table 6.10, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 6, 16, 19, 21, 25, 27, 30, 34, 36, 37, 39, 43, 44, and/or 47 of Table 6.10

is indicative for AML_M1 when AML_M1 is distinguished from AML_M5b,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 19, 22, 38, and/or 45, of Table 6.11, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 20, 21, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 39, 40, 41, 42, 43, 44, 46, 47, 48, 49, and/or 50 of Table 6.11

is indicative for AML_M1 when AML_M1 is distinguished from AML_M6,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 16, 17, 18, 20, 21, 22, 23, 24, 25, 26, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 43, 45, 46, 47, 49, and/or 50 of Table 6.12, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 14, 15, 19, 27, 40, 41, 42, 44, and/or 48 of table 6.12,

is indicative for AML_M2 when AML_M2 is distinguished from AML_M4,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 12 of Table 6.13, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 6.13

is indicative for AML_M2 when AML_M2 is distinguished from AML_M5a,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 19, 20, 21, 23, 24, 25, 26, 28, 32, 33, 34, 37, 38, 39, 40, 41, 42, 43, 44, 45, 47, 49, and/or 50 of Table 6.14, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 13, 17, 22, 27, 29, 30, 31, 35, 36, 46, and/or 48 of Table 6.14,

is indicative for AML_M2 when AML_M2 is distinguished from AML_M5b,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 26, 36, and/or 46, of Table 6.15, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 27, 28, 29, 30, 31, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 43, 44, 45, 47, 48, 49, and/or 50 of Table 6.15

is indicative for AML_M2 when AML_M2 is distinguished from AML_M6,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 18, 21, 25, 28, 29, 36, 40, 43, and/or 46, of Table 6.16, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 19, 20, 22, 23, 24, 26, 27, 30, 31, 32, 33, 34, 35, 37, 38, 39, 41, 42, 44, 45, 47, 48, 49, and/or 50 of Table 6.16

is indicative for AML_M4 when AML_M4 is distinguished from AML_M5a,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 7, 9, 10, 12, 13, 15, 18, 19, 22, 25, 26, 28, 31, 32, 33, 37, 38, 40, 42, 47, and/or 50 of Table 6.17, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 5, 6, 8, 11, 14, 16, 17, 20, 21, 23, 24, 27, 29, 30, 34, 35, 36, 39, 41, 43, 44, 45, 46, 48, and/or 49 of Table 6.17,

is indicative for AML_M4 when AML_M4 is distinguished from AML_M5b,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 39, 40, 41, and/or 47 of Table 6.18, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 42, 43, 44, 45, 46, 48, 49, and/or 50 of Table 6.18,

is indicative for AML_M4 when AML_M4 is distinguished from AML_M6,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 2, 3, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 23, 24, 26, 27, 28, 29, 31, 34, 35, 36, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 6.19, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 7, 22, 25, 30, 32, 33, and/or 37 of Table 6.19,

is indicative for AML_M5a when AML_M5a is distinguished from AML_M5b,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 15, 17, 18, 20, 23, 28, 29, 31, 37, 43, 44, 45, 46, and/or 48, of Table 6.20,

a higher expression of at least one polynucleotide defined by any of the numbers 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, 19, 21, 22, 24, 25, 26, 27, 30, 32, 33, 34, 35, 36, 38, 39, 40, 41, 42, 47, 49, and/or 50 of Table 6.20

is indicative for AML_M5a when AML_M5a is distinguished from AML_M6,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 40, and/or 48, of Table 6.21, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 41, 42, 43, 44, 45, 46, 47, 49, and/or 50 of Table 6.21

is indicative for AML_M5b when AML_M5b is distinguished from AML_M6,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 18, 19, 20, 21, 22, 23, 24, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 7, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 16, 17, and/or 25, of Table 7

is indicative for AML_M3 when AML_M3 is distinguished from AML_M3v,

As used herein, "AML subtype" refers to the subtype classification of the World Health Organization (WHO) published in 2001. Therefore, an "AML Subtype" can

be classified according to 1. recurrent genetic abnormalities e.g. (t(15;17); t(8;21); inv(3); inv(16); t(11q23)), 2. dysplastic features, 3. history of the patient: AML following MDS (myelodysplastic syndrome); s_AML, or therapy-related, t_AML; and 4. (immuno-) phenotypical differences of maturation and cell lineage composition as formerly defined in the FAB classification. AML_M1, M2, M4, M5a , M5b, M6, M3, M3v refer to subtypes (different stages) classified after their cytomorphological appearance.

As used herein, "all other subtypes" refer to the subtypes of the present invention, i.e. if one subtype is distinguished from "all other subtypes", it is distiguished from all other subtypes contained in the present invention.

According to the present invention, a "sample" means any biological material containing genetic information in the form of nucleic acids or proteins obtainable or obtained from an individual. The sample includes e.g. tissue samples, cell samples, bone marrow and/or body fluids such as blood, saliva, semen. Preferably, the sample is blood or bone marrow, more preferably the sample is bone marrow. The person skilled in the art is aware of methods, how to isolate nucleic acids and proteins from a sample. A general method for isolating and preparing nucleic acids from a sample is outlined in Example 3.

According to the present invention, the term "lower expression" is generally assigned to all by numbers and Affymetrix Id. definable polynucleotides the t-values and fold change (fc) values of which are negative, as indicated in the Tables. Accordingly, the term "higher expression" is generally assigned to all by numbers and Affymetrix Id. definable polynucleotides the t-values and fold change (fc) values of which are positive.

According to the present invention, the term "expression" refers to the process by which mRNA or a polypeptide is produced based on the nucleic acid sequence of a gene, i.e. „expression" also includes the formation of mRNA upon transcription. In accordance with the present invention, the term „determining the expression level" preferably refers to the determination of the level of expression, namely of the markers.

Generally, "marker" refers to any genetically controlled difference which can be used in the genetic analysis of a test versus a control sample, for the purpose of assigning the sample to a defined genotype or phenotype. As used herein, "markers" refer to genes which are differentially expressed in, e.g., different AML subtypes. The markers can be defined by their gene symbol name, their encoded protein name, their transcript identification number (cluster identification number), the data base accession number, public accession number or GenBank identifier or, as done in the present invention, Affymetrix identification number, chromosomal location, UniGene accession number and cluster type, LocusLink accession number (see Examples and Tables).

The Affymetrix identification number (affy id) is accessible for anyone and the person skilled in the art by entering the "gene expression omnibus" internet page of the National Center for Biotechnology Information (NCBI) (http://www.ncbi.nlm.nih.gov/geo/). In particular, the affy id's of the polynucleotides used for the method of the present invention are derived from the so-called U133 chip. The sequence data of each identification number can be viewed at http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GPL96

Generally, the expression level of a marker is determined by the determining the expression of its corresponding "polynucleotide" as described hereinafter.

According to the present invention, the term „polynucleotide" refers, generally, to a DNA, in particular cDNA, or RNA, in particular a cRNA, or a portion thereof or a polypeptide or a portion thereof. In the case of RNA (or cDNA), the polynucleotide is formed upon transcription of a nucleotide sequence which is capable of expression. The polynucleotide fragments refer to fragments preferably of between at least 8, such as 10, 12, 15 or 18 nucleotides and at least 50, such as 60, 80, 100, 200 or 300 nucleotides in length, or a complementary sequence thereto, representing a consecutive stretch of nucleotides of a gene, cDNA or mRNA. In other terms, polynucleotides include also any fragment (or complementary sequence thereto) of a sequence derived from any of the markers defined above as long as these fragments unambiguously identify the marker.

The determination of the expression level may be effected at the transcriptional or translational level, i.e. at the level of mRNA or at the protein level. Protein fragments such as peptides or polypeptides advantageously comprise between at least 6 and at least 25, such as 30, 40, 80, 100 or 200 consecutive amino acids representative of the corresponding full length protein. Six amino acids are generally recognized as the lowest peptidic stretch giving rise to a linear epitope recognized by an antibody, fragment or derivative thereof. Alternatively, the proteins or fragments thereof may be analysed using nucleic acid molecules specifically binding to three-dimensional structures (aptamers).

Depending on the nature of the polynucleotide or polypeptide, the determination of the expression levels may be effected by a variety of methods. For determining and detecting the expression level, it is preferred in the present invention that the polynucleotide, in particular the cRNA, is labelled.

The labelling of the polynucleotide or a polypeptide can occur by a variety of methods known to the skilled artisan. The label can be fluorescent, chemiluminescent, bioluminescent, radioactive (such as ^{3}H or ^{32}P). The labelling compound can be any labelling compound being suitable for the labelling of polynucleotides and/or polypeptides. Examples include fluorescent dyes, such as fluorescein, dichlorofluorescein, hexachlorofluorescein, BODIPY variants, ROX, tetramethylrhodamin, rhodamin X, Cyanine-2, Cyanine-3, Cyanine-5, Cyanine-7, IRD40, FluorX, Oregon Green, Alexa variants (available e.g. from Molecular Probes or Amersham Biosciences) and the like, biotin or biotinylated nucleotides, digoxigenin, radioisotopes, antibodies, enzymes and receptors. Depending on the type of labelling, the detection is done via fluorescence measurements, conjugation to streptavidin and/or avidin, antigen-antibody- and/or antibody-antibody-interactions, radioactivity measurements, as well as catalytic and/or receptor/ligand interactions. Suitable methods include the direct labelling (incorporation) method, the amino-modified (amino-allyl) nucleotide method (available e.g. from Ambion), and the primer tagging method (DNA dendrimer labelling, as kit available e.g. from Genisphere). Particularly preferred for the present invention is the use of biotin or biotinylated nucleotides for labelling, with the latter being directly incorporated into, e.g. the cRNA polynucleotide by in vitro transcription.

If the polynucleotide is mRNA, cDNA may be prepared into which a detectable label, as exemplified above, is incorporated. Said detectably labelled cDNA, in single-stranded form, may then be hybridised, preferably under stringent or highly stringent conditions to a panel of single-stranded oligonucleotides representing different genes and affixed to a solid support such as a chip. Upon applying appropriate washing steps, those cDNAs will be detected or quantitatively detected that have a counterpart in the oligonucleotide panel. Various advantageous embodiments of this general method are feasible. For example, the mRNA or the cDNA may be amplified e.g. by polymerase chain reaction, wherein it is preferable, for quantitative assessments, that the number of amplified copies corresponds relative to further amplified mRNAs or cDNAs to the number of mRNAs originally present in the cell. In a preferred embodiment of the present invention, the cDNAs are transcribed into cRNAs prior to the hybridisation step wherein only in the transcription step a label is incorporated into the nucleic acid and wherein the cRNA is employed for hybridisation. Alternatively, the label may be attached subsequent to the transcription step.

Similarly, proteins from a cell or tissue under investigation may be contacted with a panel of aptamers or of antibodies or fragments or derivatives thereof. The antibodies etc. may be affixed to a solid support such as a chip. Binding of proteins indicative of an AML subtype may be verified by binding to a detectably labelled secondary antibody or aptamer. For the labelling of antibodies, it is referred to Harlow and Lane, "Antibodies, a laboratory manual", CSH Press, 1988, Cold Spring Harbor. Specifically, a minimum set of proteins necessary for diagnosis of all AML subtypes may be selected for creation of a protein array system to make diagnosis on a protein lysate of a diagnostic bone marrow sample directly. Protein Array Systems for the detection of specific protein expression profiles already are available (for example: Bio-Plex, BIORAD, München, Germany). For this application preferably antibodies against the proteins have to be produced and immobilized on a platform e.g. glasslides or microtiterplates. The immobilized antibodies can be labelled with a reactant specific for the certain target proteins as discussed above. The reactants can include enzyme substrates, DNA, receptors, antigens or antibodies to create for example a capture sandwich immunoassay.

For reliably distinguishing AML subtypes it is useful that the expression of more than one of the above defined markers is determined. As a criterion for the choice of markers, the statistical significance of markers as expressed in q or p values based on the concept of the false discovery rate is determined. In doing so, a measure of statistical significance called the q value is associated with each tested feature. The q value is similar to the p value, except it is a measure of significance in terms of the false discovery rate rather than the false positive rate (Storey JD and Tibshirani R. Proc.Natl.Acad.Sci., 2003, Vol. 100:9440-5.

In a preferred embodiment of the present invention, markers as defined in Tables 1-7 having a q-value of less than 3E-06, more preferred less than 1.5E-09, most preferred less than 1.5E-11, less than 1.5E-20, less than 1.5E-30, are measured.

Of the above defined markers, the expression level of at least two, preferably of at least ten, more preferably of at least 25, most preferably of 50 of at least one of the Tables of the markers is determined.

In another preferred embodiment, the expression level of at least 2, of at least 5, of at least 10 out of the markers having the numbers 1 – 10, 1-20, 1-40, 1-50 of at least one of the Tables are measured.

The level of the expression of the „marker", i.e. the expression of the polynucleotide is indicative of the AML subtype of a cell or an organism. The level of expression of a marker or group of markers is measured and is compared with the level of expression of the same marker or the same group of markers from other cells or samples. The comparison may be effected in an actual experiment or in silico. When the expression level also referred to as expression pattern or expression signature (expression profile) is measurably different, there is according to the invention a meaningful difference in the level of expression. Preferably the difference at least is 5 %, 10% or 20%, more preferred at least 50% or may even be as high as 75% or 100%. More preferred the difference in the level of expression is at least 200%, i.e. two fold, at least 500%, i.e. five fold, or at least 1000%, i.e. 10 fold.

Accordingly, the expression level of markers expressed lower in a first subtype than in at least one second subtype, which differs from the first subtype, is at least

5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold lower, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold lower in the first subtype. On the other hand, the expression level of markers expressed higher in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold higher, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold higher in the first subtype.

In another embodiment of the present invention, the sample is derived from an individual having leukaemia, preferably AML.

For the method of the present invention it is preferred if the polynucleotide the expression level of which is determined is in form of a transcribed polynucleotide. A particularly preferred transcribed polynucleotide is an mRNA, a cDNA and/or a cRNA, with the latter being preferred. Transcribed polynucleotides are isolated from a sample, reverse transcribed and/or amplified, and labelled, by employing methods well-known the person skilled in the art (see Example 3). In a preferred embodiment of the methods according to the invention, the step of determining the expression profile further comprises amplifying the transcribed polynucleotide.

In order to determine the expression level of the transcribed polynucleotide by the method of the present invention, it is preferred that the method comprises hybridizing the transcribed polynucleotide to a complementary polynucleotide, or a portion thereof, under stringent hybridization conditions, as described hereinafter.

The term "hybridizing" means hybridization under conventional hybridization conditions, preferably under stringent conditions as described, for example, in Sambrook, J., et al., in "Molecular Cloning: A Laboratory Manual" (1989), Eds. J. Sambrook, E. F. Fritsch and T. Maniatis, Cold Spring Harbour Laboratory Press, Cold Spring Harbour, NY and the further definitions provided above. Such conditions are, for example, hybridization in 6x SSC, pH 7.0 / 0.1% SDS at about 45°C for 18-23 hours, followed by a washing step with 2x SSC/0.1% SDS at 50°C. In order to select the stringency, the salt concentration in the washing step can for example be chosen between 2x SSC/0.1% SDS at room temperature for low stringency and 0.2x SSC/0.1% SDS at 50°C for high stringency. In addition, the temperature of the washing step can be varied between room temperature, ca. 22°C,

for low stringency, and 65°C to 70° C for high stringency. Also contemplated are polynucleotides that hybridize at lower stringency hybridization conditions. Changes in the stringency of hybridization and signal detection are primarily accomplished through the manipulation, preferably of formamide concentration (lower percentages of formamide result in lowered stringency), salt conditions, or temperature. For example, lower stringency conditions include an overnight incubation at 37°C in a solution comprising 6X SSPE (20X SSPE = 3M NaCl; 0.2M NaH2PO4; 0.02M EDTA, pH 7.4), 0.5% SDS, 30% formamide, 100 mg/ml salmon sperm blocking DNA, followed by washes at 50°C with 1 X SSPE, 0.1% SDS. In addition, to achieve even lower stringency, washes performed following stringent hybridization can be done at higher salt concentrations (e.g. 5x SSC). Variations in the above conditions may be accomplished through the inclusion and/or substitution of alternate blocking reagents used to suppress background in hybridization experiments. The inclusion of specific blocking reagents may require modification of the hybridization conditions described above, due to problems with compatibility.

"Complementary" and "complementarity", respectively, can be described by the percentage, i.e. proportion, of nucleotides which can form base pairs between two polynucleotide strands or within a specific region or domain of the two strands. Generally, complementary nucleotides are, according to the base pairing rules, adenine and thymine (or adenine and uracil), and cytosine and guanine. Complementarity may be partial, in which only some of the nucleic acids' bases are matched according to the base pairing rules. Or, there may be a complete or total complementarity between the nucleic acids. The degree of complementarity between nucleic acid strands has effects on the efficiency and strength of hybridization between nucleic acid strands.

Two nucleic acid strands are considered to be 100% complementary to each other over a defined length if in a defined region all adenines of a first strand can pair with a thymine (or an uracil) of a second strand, all guanines of a first strand can pair with a cytosine of a second strand, all thymine (or uracils) of a first strand can pair with an adenine of a second strand, and all cytosines of a first strand can pair with a guanine of a second strand, and vice versa. According to the present invention, the degree of complementarity is determined over a stretch of 20, preferably 25, nucleotides, i.e. a 60% complementarity means that within a region of 20 nucleotides of two nucleic acid strands 12 nucleotides of the first strand can

base pair with 12 nucleotides of the second strand according to the above ruling,
either as a stretch of 12 contiguous nucleotides or interspersed by non-pairing
nucleotides, when the two strands are attached to each other over said region of 20
nucleotides. The degree of complementarity can range from at least about 50% to
5   full, i.e. 100% complementarity. Two single nucleic acid strands are said to be
"substantially complementary" when they are at least about 80% complementary,
preferably about 90% or higher. For carrying out the method of the present
invention substantial complementarity is preferred.

10   Preferred methods for detection and quantification of the amount of
polynucleotides, i.e. for the methods according to the invention allowing the
determination of the level of expression of a marker, are those described by
Sambrook et al. (1989) or real time methods known in the art as the TaqMan®
method disclosed in WO92/02638 and the corresponding U.S. 5,210,015, U.S.
15   5,804,375, U.S. 5,487,972. This method exploits the exonuclease activity of a
polymerase to generate a signal. In detail, the (at least one) target nucleic acid
component is detected by a process comprising contacting the sample with an
oligonucleotide containing a sequence complementary to a region of the target
nucleic acid component and a labeled oligonucleotide containing a sequence
20   complementary to a second region of the same target nucleic acid component
sequence strand, but not including the nucleic acid sequence defined by the first
oligonucleotide, to create a mixture of duplexes during hybridization conditions,
wherein the duplexes comprise the target nucleic acid annealed to the first
oligonucleotide and to the labeled oligonucleotide such that the 3'-end of the first
25   oligonucleotide is adjacent to the 5'-end of the labeled oligonucleotide. Then this
mixture is treated with a template-dependent nucleic acid polymerase having a 5'
to 3' nuclease activity under conditions sufficient to permit the 5' to 3' nuclease
activity of the polymerase to cleave the annealed, labeled oligonucleotide and
release labeled fragments. The signal generated by the hydrolysis of the labeled
30   oligonucleotide is detected and/ or measured. TaqMan® technology eliminates the
need for a solid phase bound reaction complex to be formed and made detectable.
Other methods include e.g. fluorescence resonance energy transfer between two
adjacenly hybridized probes as used in the LightCycler® format described in U.S.
6,174,670.

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A preferred protocol if the marker, i.e. the polynucleotide, is in form of a transcribed nucleotide, is described in Example 3, where total RNA is isolated, cDNA and, subsequently, cRNA is synthesized and biotin is incorporated during the transcription reaction. The purified cRNA is applied to commercially available arrays which can be obtained e.g. from Affymetrix. The hybridized cRNA is detected according to the methods described in Example 3. The arrays are produced by photolithography or other methods known to experts skilled in the art e.g. from U.S. 5,445,934, U.S. 5,744,305, U.S. 5,700,637, U.S. 5,945,334 and EP 0 619 321 or EP 0 373 203, or as decribed hereinafter in greater detail.

In another embodiment of the present invention, the polynucleotide or at least one of the polynucleotides is in form of a polypeptide. In another preferred embodiment, the expression level of the polynucleotides or polypeptides is detected using a compound which specifically binds to the polynucleotide of the polypeptide of the present invention.

As used herein, "specifically binding" means that the compound is capable of discriminating between two or more polynucleotides or polypeptides, i.e. it binds to the desired polynucleotide or polypeptide, but essentially does not bind unspecifically to a different polynucleotide or polypeptide.

The compound can be an antibody, or a fragment thereof, an enzyme, a so-called small molecule compound, a protein-scaffold, preferably an anticalin. In a preferred embodiment, the compound specifically binding to the polynucleotide or polypeptide is an antibody, or a fragment thereof.

As used herein, an "antibody" comprises monoclonal antibodies as first described by Köhler and Milstein in Nature 278 (1975), 495-497 as well as polyclonal antibodies, i.e. entibodies contained in a polyclonal antiserum. Monoclonal antibodies include those produced by transgenic mice. Fragments of antibodies include F(ab')₂, Fab and Fv fragments. Derivatives of antibodies include scFvs, chimeric and humanized antibodies. See, for example Harlow and Lane, loc. cit. For the detection of polypeptides using antibodies or fragments thereof, the person skilled in the art is aware of a variety of methods, all of which are included in the present invention. Examples include immunoprecipitation, Western blotting,

Enzyme-linked immuno sorbent assay (ELISA), Enzyme-linked immuno sorbent assay (RIA), dissociation-enhanced lanthanide fluoro immuno assay (DELFIA), scintillation proximity assay (SPA). For detection, it is desirable if the antibody is labelled by one of the labelling compounds and methods described supra.

In another preferred embodiment of the present invention, the method for distinguishing WHO- classified AML subtypes is carried out on an array.

In general, an "array" or "microarray" refers to a linear or two- or three dimensional arrangement of preferably discrete nucleic acid or polypeptide probes which comprises an intentionally created collection of nucleic acid or polypeptide probes of any length spotted onto a substrate/solid support. The person skilled in the art knows a collection of nucleic acids or polypeptide spotted onto a substrate/solid support also under the term "array". As known to the person skilled in the art, a microarray usually refers to a miniaturised array arrangement, with the probes being attached to a density of at least about 10, 20, 50, 100 nucleic acid molecules referring to different or the same genes per cm^2. Furthermore, where appropriate an array can be referred to as "gene chip". The array itself can have different formats, e.g. libraries of soluble probes or libraries of probes tethered to resin beads, silica chips, or other solid supports.

The process of array fabrication is well-known to the person skilled in the art. In the following, the process for preparing a nucleic acid array is described. Commonly, the process comprises preparing a glass (or other) slide (e.g. chemical treatment of the glass to enhance binding of the nucleic acid probes to the glass surface), obtaining DNA sequences representing genes of a genome of interest, and spotting sequences these sequences of interest onto glass slide. Sequences of interest can be obtained via creating a cDNA library from an mRNA source or by using publicly available databases, such as GeneBank, to annotate the sequence information of custom cDNA libraries or to identify cDNA clones from previously prepared libraries. Generally, it is recommendable to amplify obtained sequences by PCR in order to have sufficient amounts of DNA to print on the array. The liquid containing the amplified probes can be deposited on the array by using a set of microspotting pins. Ideally, the amount deposited should be uniform. The process can further include UV-crosslinking in order to enhance immobilization of the probes on the array.

In a preferred embodiment, the array is a high density oligonucleotide (oligo) array using a light-directed chemical synthesis process, employing the so-called photolithography technology. Unlike common cDNA arrays, oligo arrays (according to the Affymetrix technology) use a single-dye technology. Given the sequence information of the markers, the sequence can be synthesized directly onto the array, thus, bypassing the need for physical intermediates, such as PCR products, required for making cDNA arrays. For this purpose, the marker, or partial sequences thereof, can be represented by 14 to 20 features, preferably by less than 14 features, more preferably less than 10 features, even more preferably by 6 features or less, with each feature being a short sequence of nucleotides (oligonucleotide), which is a perfect match (PM) to a segment of the respective gene. The PM oligonucleotide are paired with mismatch (MM) oligonucleotides which have a single mismatch at the central base of the nucleotide and are used as "controls". The chip exposure sites are defined by masks and are deprotected by the use of light, followed by a chemical coupling step resulting in the synthesis of one nucleotide. The masking, light deprotection, and coupling process can then be repeated to synthesize the next nucleotide, until the nucleotide chain is of the specified length.

Advantageously, the method of the present invention is carried out in a robotics system including robotic plating and a robotic liquid transfer system, e.g. using microfluidics, i.e. channelled structured.

A particular preferred method according to the present invention is as follows:
1. Obtaining a sample, e.g. bone marrow aliquots, from a patient having AML
2. Extracting RNA, preferably mRNA, from the sample
3. Reverse transcribing the RNA into cDNA
4. In vitro transcribing the cDNA into cRNA
5. Fragmenting the cRNA
6. Hybridizing the fragmented cRNA on standard microarrays
7. Determining hybridization

In another embodiment, the present invention is directed to the use of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, 3, 4, 5, 6 and/or 7 for the manufacturing of a diagnostic for distinguishing WHO classified AML subtypes.

The use of the present invention is particularly advantageous for distinguishing WHO classified AML subtypes in an individual having AML. The use of said markers for diagnosis of WHO classified leukemia subtypes, preferably based on microarray technology, offers the following advantages: (1) more rapid and more precise diagnosis, (2) easy to use in laboratories without specialized experience, (3) abolishes the requirement for analyzing viable cells for chromosome analysis (transport problem), and (4) very experienced hematologists for cytomorphology and cytochemistry, immunophenotyping as well as cytogeneticists and molecularbiologists are no longer required.

Accordingly, the present invention refers to a diagnostic kit containing at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, 3, 4, 5, 6 and/or 7 for distinguishing WHO classified AML subtypes, in combination with suitable auxiliaries. Suitable auxiliaries, as used herein, include buffers, enzymes, labelling compounds, and the like. In a preferred embodiment, the marker contained in the kit is a nucleic acid molecule which is capable of hybridizing to the mRNA corresponding to at least one marker of the present invention. Preferably, the at least one nucleic acid molecule is attached to a solid support, e.g. a polystyrene microtiter dish, nitrocellulose membrane, glass surface or to non-immobilized particles in solution.

In another preferred embodiment, the diagnostic kit contains at least one reference for a AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a, AML_M5b, AML_M6, AML_t(15;17)/M3 and/or AML_t(15;17)/M3v subtype. As used herein, the reference can be a sample or a data bank.

In another embodiment, the present invention is directed to an apparatus for distinguishing WHO classified AML subtypes AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a, AML_M5b, AML_M6, AML_t(15;17)/M3 and/or AML_t(15;17)/M3v in a sample, containing a reference data bank obtainable by comprising

  (a) compiling a gene expression profile of a patient sample by determining the expression level at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, 3, 4, 5, 6 and/or 7, and

(b) classifying the gene expression profile by means of a machine learning algorithm.

According to the present invention, the "machine learning algorithm" is a computational-based prediction methodology, also known to the person skilled in the art as "classifier", employed for characterizing a gene expression profile. The signals corresponding to a certain expression level which are obtained by the microarray hybridization are subjected to the algorithm in order to classify the expression profile. Supervised learning involves "training" a classifier to recognize the distinctions among classes and then "testing" the accuracy of the classifier on an independent test set. For new, unknown sample the classifier shall predict into which class the sample belongs.

Preferably, the machine learning algorithm is selected from the group consisting of Weighted Voting, K-Nearest Neighbors, Decision Tree Induction, Support Vector Machines (SVM), and Feed-Forward Neural Networks. Most preferably, the machine learning algorithm is Support Vector Machine, such as polynomial kernel and Gaussian Radial Basis Function-kernel SVM models.

The classification accuracy of a given gene list for a set of microarray experiments is preferably estimated using Support Vector Machines (SVM), because there is evidence that SVM-based prediction slightly outperforms other classification techniques like k-Nearest Neighbors (k-NN). The LIBSVM software package version 2.36 was used (SVM-type: C-SVC, linear kernel (http://www.csie.ntu.edu.tw/~cjlin/libsvm/)). The skilled artisan is furthermore referred to Brown et al., Proc.Natl.Acad.Sci., 2000; 97: 262-267, Furey et al., Bioinformatics. 2000; 16: 906-914, and Vapnik V. Statistical Learning Theory. New York: Wiley, 1998.

In detail, the classification accuracy of a given gene list for a set of microarray experiments can be estimated using Support Vector Machines (SVM) as supervised learning technique. Generally, SVMs are trained using differentially expressed genes which were identified on a subset of the data and then this trained model is employed to assign new samples to those trained groups from a second and different data set. Differentially expressed genes were identified applying ANOVA and t-test-statistics (Welch t-test). Based on identified distinct gene expression

signatures respective training sets consisting of 2/3 of cases and test sets with 1/3 of cases to assess classification accuracies are designated. Assignment of cases to training and test set is randomized and balanced by diagnosis. Based on the training set a Support Vector Machine (SVM) model is built.

According to the present invention, the apparent accuracy, i.e. the overall rate of correct predictions of the complete data set was estimated by 10fold cross validation. This means that the data set was divided into 10 approximately equally sized subsets, an SVM-model was trained for 9 subsets and predictions were generated for the remaining subset. This training and prediction process was repeated 10 times to include predictions for each subset. Subsequently the data set was split into a training set, consisting of two thirds of the samples, and a test set with the remaining one third. Apparent accuracy for the training set was estimated by 10fold cross validation (analogous to apparent accuracy for complete set). A SVM-model of the training set was built to predict diagnosis in the independent test set, thereby estimating true accuracy of the prediction model. This prediction approach was applied both for overall classification (multi-class) and binary classification (diagnosis X => yes or no). For the latter, sensitivity and specificity were calculated:

Sensitivity = (number of positive samples predicted)/(number of true positives)

Specificity = (number of negative samples predicted)/(number of true negatives)

In a preferred embodiment, the reference data bank is backed up on a computational data memory chip which can be inserted in as well as removed from the apparatus of the present invention, e.g. like an interchangeable module, in order to use another data memory chip containing a different reference data bank.

The apparatus of the present invention containing a desired reference data bank can be used in a way such that an unknown sample is, first, subjected to gene expression profiling, e.g. by microarray analysis in a manner as described supra or in the art, and the expression level data obtained by the analysis are, second, fed into the apparatus and compared with the data of the reference data bank obtainable by the above method. For this purpose, the apparatus suitably contains a device for entering the expression level of the data, for example a control panel such as a keyboard. The results, whether and how the data of the unknown sample fit into the

reference data bank can be made visible on a provided monitor or display screen and, if desired, printed out on an incorporated of connected printer.

Alternatively, the apparatus of the present invention is equipped with particular appliances suitable for detecting and measuring the expression profile data and, subsequently, proceeding with the comparison with the reference data bank. In this embodiment, the apparatus of the present invention can contain a gripper arm and/or a tray which takes up the microarray containing the hybridized nucleic acids.

In another embodiment, the present invention refers to a reference data bank for distinguishing AML subtypes AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a, AML_M5b, AML_M6, AML_t(15;17)/M3 and AML_t(15;17)/M3v in a sample obtainable by comprising

        (a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, 3, 4, 5, 6 and/or 7, and

        (b) classifying the gene expression profile by means of a machine learning algorithm.

Preferably, the reference data bank is backed up and/or contained in a computational memory data chip.

The invention is further illustrated in the following table and examples, without limiting the scope of the invention:

TABLES 1-7

Tables 1-7 show AML subtype analysis of AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a, AML_M5b, AML_M6, AML_t(15;17)/M3 and AML_t(15;17)/M3v. The analysed markers are ordered according to their q-values, beginning with the lowest q-values.

For convenience and a better understanding, Tables 1 to 7 are accompanied with explanatory tables (Table 1A to 7A) where the numbering and the Affymetrix Id are further defined by other parameters, e.g. gene bank accession number.

EXAMPLES

Example 1:   General experimental design of the invention and results

366 patients with AML at diagnosis by cytomorphology, immunophenotyping, cytogenetics, and gene expression profiling addressing 33,000 genes (U133 set, Affymetrix) were investigated. Microarray data was analyzed by pattern recognition algorithms (Principal Component Analysis (PCA), and hierarchical clustering). To identify differentially expressed genes ANOVA and t-test-statistics (Welch t-test) was applied. To assess the false discovery rate, q values according to Storey (PNAS, 2003, supra) werecalculated. To estimate diagnostic accuracy based on gene expression signatures, a training set consisting of 2/3 of cases and a test set with 1/3 of cases was built. Assignment of cases to training and test set was randomized and balanced by diagnosis. For estimation of classification accuracies a SVM model was built based on the training set. Classification accuracies were assessed in the test set. Following the first step of WHO hierarchy all cases with t(15;17) (n=20); t(8;21) (n=25); inv(16) (n=25); or 11q23 (n=33) with 100% accuracy were identified. After adding the 263 "other AML" cases to total cohort, in the test set 120/122 (98%) AML samples were correctly assigned. Approaching the history of the leukemia: In the whole cohort 334 patients were de novo AML,

11 had AML following MDS, and 21 were therapy-related AML. For these three groups the test set comprised 122 patients, out of which 108 were correctly assigned to the respective subgroup based on gene expression data (accuracy 89%). A subset of 221 patients encompasses those cases that do not fulfill criteria for inclusion in one of the previously described WHO groups. Therefore, we attempted to reproduce the immunologically defined subtype formerly addressed by FAB as M0 (n=15), and all morphological subcategories formely addressed as M1 (n=66), M2 (n=67), M4 (n=36), M5a (n=11), M5b (n=17), or M6 (n=9). The test set included 73 patients. As morphological criterias according to FAB thresholds werearbitrary and reproducibility even between experienced cytomorphologists was only 55-80%, it was expected to achieve only limited accuracies for these categories also with respect to gene expression data. As such, 51 of 73 cases (56%) of the test set were correctly assigned. In 8 cases misclassification occurred between M1 and M2, also M4 cases were incorrectly assigned into M2. Therefore, it can be presumed that AML M2 was the most heterogeneous subtype covering a variety of different biological entities. In contrast, all cases with M5b were correctly identified suggesting that this is the most homogeneous morphological subgroup. In addition, it was possible to separate AML with t(15;17) into the cytomorphological subtypes M3 (n=10) and M3v (n=10) by specific gene expression profiles with an accuracy of 100%. In conclusion, the WHO classification of AML mainly reflects distinct biological entities as described by genetic features, history of the leukemia, and immunophenotype or phenotype of the malignant cells. This can also clearly be reproduced by underlying gene expression patterns. Furthermore, this expression data may be the basis for a more accurate and reproducible subclassification system of AML.

Example 2: General materials, methods and definitions of functional annotations

The methods section contains both information on statistical analyses used for identification of differentially expressed genes and detailed annotation data of identified microarray probesets.

<u>Affymetrix Probeset Annotation</u>
All annotation data of GeneChip® arrays are extracted from the NetAffx™
Analysis Center (internet website: www.affymetrix.com). Files for U133 set arrays,
including U133A and U133B microarrays are derived from the June 2003 release.

5   The original publication refers to: Liu G, Loraine AE, Shigeta R, Cline M, Cheng J,
Valmeekam V, Sun S, Kulp D, Siani-Rose MA. NetAffx: Affymetrix probesets and
annotations. Nucleic Acids Res. 2003;31(1):82-6.

The sequence data are omitted due to their large size, and because they do not

10   change, whereas the annotation data are updated periodically, for example new
information on chromomal location and functional annotation of the respective
gene products. Sequence data are available for download in the NetAffx Download
Center (www.affymetrix.com)

15   Data fields:
In the following section, the content of each field of the data files are described.
Microarray probesets, for example found to be differentially expressed between
different types of leukemia samples are further described by additional information.
The fields are of the following types:

20

1. GeneChip Array Information
2. Probe Design Information
3. Public Domain and Genomic References

25   1. GeneChip Array Information

HG-U133 ProbeSet_ID:
HG-U133 ProbeSet_ID describes the probe set identifier. Examples are:
200007_at, 200011_s_at, 200012_x_at.

30

GeneChip:
The description of the GeneChip probe array name where the respective probeset is
represented. Examples are: Affymetrix Human Genome U133A Array or
Affymetrix Human Genome U133B Array.

35

2. Probe Design Information

Sequence Type:

The Sequence Type indicates whether the sequence is an Exemplar, Consensus or

5   Control sequence. An Exemplar is a single nucleotide sequence taken directly from
a public database. This sequence could be an mRNA or EST. A Consensus
sequence, is a nucleotide sequence assembled by Affymetrix, based on one or more
sequence taken from a public database.

10   Transcript ID:

The cluster identification number with a sub-cluster identifier appended.

Sequence Derived From:

The accession number of the single sequence, or representative sequence on which

15   the probe set is based. Refer to the "Sequence Source" field to determine the
database used.

Sequence ID:

For Exemplar sequences: Public accession number or GenBank identifier. For

20   Consensus sequences: Affymetrix identification number or public accession
number.

Sequence Source:

The database from which the sequence used to design this probe set was taken.

25   Examples are: GenBank®, RefSeq, UniGene, TIGR (annotations from The
Institute for Genomic Research).

3. Public Domain and Genomic References

30   Most of the data in this section come from LocusLink and UniGene databases, and
are annotations of the reference sequence on which the probe set is modeled.

Gene Symbol and Title:

A gene symbol and a short title, when one is available. Such symbols are assigned

35   by different organizations for different species. Affymetrix annotational data come
from the UniGene record. There is no indication which species-specific databank

was used, but some of the possibilities include for example HUGO: The Human Genome Organization.

MapLocation:

The map location describes the chromosomal location when one is available.

Unigene_Accession:

UniGene accession number and cluster type. Cluster type can be "full length" or "est", or "---" if unknown.

LocusLink:

This information represents the LocusLink accession number.

Full Length Ref. Sequences:

Indicates the references to multiple sequences in RefSeq. The field contains the ID and description for each entry, and there can be multiple entries per probeSet.

Example 3:   Sample preparation, processing and data analysis

Method 1:

Microarray analyses were performed utilizing the GeneChip® System (Affymetrix, Santa Clara, USA). Hybridization target preparations were performed according to recommended protocols (Affymetrix Technical Manual). In detail, at time of diagnosis, mononuclear cells were purified by Ficoll-Hypaque density centrifugation. They had been lysed immediately in RLT buffer (Qiagen, Hilden, Germany), frozen, and stored at -80°C from 1 week to 38 months. For gene expression profiling cell lysates of the leukemia samples were thawed, homogenized (QIAshredder, Qiagen), and total RNA was extracted (RNeasy Mini Kit, Qiagen). Subsequently, 5-10 µg total RNA isolated from 1×10^7 cells was used as starting material for cDNA synthesis with oligo[(dT)$_{24}$T7promotor]$_{65}$ primer (cDNA Synthesis System, Roche Applied Science, Mannheim, Germany). cDNA products were purified by phenol/chlorophorm/IAA extraction (Ambion, Austin, USA) and acetate/ethanol-precipitated overnight. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides were incorporated during the following *in vitro* transcription reaction (Enzo BioArray HighYield RNA Transcript Labeling Kit, Enzo Diagnostics). After quantification by spectrophotometric measurements and 260/280 absorbance values assessment for

quality control of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 µg cRNA was fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2/500 mM potassium acetate/150 mM magnesium acetate) and added to the hybridization cocktail sufficient for five hybridizations on standard GeneChip microarrays (300 µl final volume). Washing and staining of the probe arrays was performed according to the recommended Fluidics Station protocol (EukGE-WS2v4). Affymetrix Microarray Suite software (version 5.0.1) extracted fluorescence signal intensities from each feature on the microarrays as detected by confocal laser scanning according to the manufacturer's recommendations.

Expression analysis quality assessment parameters included visiual array inspection of the scanned image for the presence of image artifacts and correct grid alignment for the identification of distinct probe cells as well as both low 3'/5' ratio of housekeeping controls (mean: 1.90 for GAPDH) and high percentage of detection calls (mean: 46.3% present called genes). The 3' to 5' ratio of GAPDH probesets can be used to assess RNA sample and assay quality. Signal values of the 3' probe sets for GAPDH are compared to the Signal values of the corresponding 5' probe set. The ratio of the 3' probe set to the 5' probe set is generally no more than 3.0. A high 3' to 5' ratio may indicate degraded RNA or inefficient synthesis of ds cDNA or biotinylated cRNA (GeneChip® Expression Analysis Technical Manual, www.affymetrix.com). Detection calls are used to determine whether the transcript of a gene is detected (present) or undetected (absent) and were calculated using default parameters of the Microarray Analysis Suite MAS 5.0 software package.

Method 2:

Bone marrow (BM) aspirates are taken at the time of the initial diagnostic biopsy and remaining material is immediately lysed in RLT buffer (Qiagen), frozen and stored at -80 C until preparation for gene expression analysis. For microarray analysis the GeneChip System (Affymetrix, Santa Clara, CA, USA) is used. The targets for GeneChip analysis are prepared according to the current Expression Analysis. Briefly, frozen lysates of the leukemia samples are thawed, homogenized (QIAshredder, Qiagen) and total RNA extracted (RNeasy Mini Kit, Qiagen).Normally 10 ug total RNA isolated from 1 x 107 cells is used as starting material in the subsequent cDNA-Synthesis using Oligo-dT-T7-Promotor Primer (cDNA synthesis Kit, Roche Molecular Biochemicals). The cDNA is purified by

phenol-chlorophorm extraction and precipitated with 100% Ethanol over night. For detection of the hybridized target nucleic acid biotin-labeled ribonucleotides are incorporated during the in vitro transcription reaction (Enzo® BioArray™ HighYield™ RNA Transcript Labeling Kit, ENZO). After quantification of the purified cRNA (RNeasy Mini Kit, Qiagen), 15 ug are fragmented by alkaline treatment (200 mM Tris-acetate, pH 8.2, 500 mM potassium acetate, 150 mM magnesium acetate) and added to the hybridization cocktail sufficient for 5 hybridizations on standard GeneChip microarrays. Before expression profiling Test3 Probe Arrays (Affymetrix) are chosen for monitoring of the integrity of the cRNA. Only labeled cRNA-cocktails which showed a ratio of the measured intensity of the 3' to the 5' end of the GAPDH gene less than 3.0 are selected for subsequent hybridization on HG-U133 probe arrays (Affymetrix). Washing and staining the Probe arrays is performed as described (siehe Affymetrix-Original-Literatur (LOCKHART und LIPSHUTZ). The Affymetrix software (Microarray Suite, Version 4.0.1) extracted fluorescence intensities from each element on the arrays as detected by confocal laser scanning according to the manufacturers recommendations.

Table 1
One-Versus-All (OVA)

1.1	AML_MLL versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	226517_at	BCAT1	-7.87	3.85E-45	8.65E-41	-0.89	-16.83	12pter-q12
2	225344_at	ERAP140	-3.72	3.36E-38	1.89E-34	-0.87	-15.87	6q22.33
3	211137_s_at	ATP2C1	-2.16	1.11E-36	4.15E-33	-0.87	-15.76	3q21-q24
4	205453_at	HOXB2	-7.93	2.57E-34	7.22E-31	-0.86	-15.34	17q21-q22
5	202746_at	ITM2A	-7.57	6.71E-38	3.02E-34	-0.82	-15.19	Xq13.3-Xq21.2
6	213258_at		-8.13	3.38E-40	3.80E-36	-0.79	-15.14	
7	205624_at	CPA3	-11.48	1.25E-39	9.36E-36	-0.78	-14.93	3q21-q25
8	201830_s_at	NET1	-3.53	1.48E-30	2.77E-27	-0.85	-14.87	10p15
9	220306_at	FLJ20202	-3.63	7.16E-30	9.47E-27	-0.81	-14.32	1p11.1
10	202747_s_at	ITM2A	-7.60	1.13E-32	2.53E-29	-0.77	-14.16	Xq13.3-Xq21.2
11	206761_at	TACTILE	-11.67	2.20E-35	7.08E-32	-0.73	-13.92	3q13.13
12	213549_at	PRO2730	-3.04	8.86E-30	1.11E-26	-0.77	-13.77	3p21.31
13	200923_at	LGALS3BP	-6.91	2.70E-33	6.74E-30	-0.70	-13.38	17q25
14	214390_s_at	BCAT1	-6.14	2.34E-30	4.05E-27	-0.73	-13.37	12pter-q12
15	201829_at	NET1	-2.33	5.34E-26	4.00E-23	-0.77	-13.34	10p15
16	208116_s_at	MAN1A1	-3.76	5.86E-30	8.79E-27	-0.72	-13.29	6q22
17	225285_at		-6.49	1.28E-25	8.49E-23	-0.77	-13.24	
18	225831_at	LOC148894	-3.00	6.99E-24	3.66E-21	-0.79	-13.21	1p36.11
19	225532_at	LOC91768	-2.87	2.82E-28	3.17E-25	-0.72	-13.08	18q11.1
20	219188_s_at	LRP16	-3.35	3.93E-26	3.05E-23	-0.74	-13.03	11q11
21	221760_at	MAN1A1	-4.97	6.33E-31	1.29E-27	-0.69	-13.01	6q22
22	205601_s_at	HOXB5	-2.51	3.82E-30	6.14E-27	-0.69	-12.87	17q21.3
23	236513_at		-2.53	1.20E-25	8.16E-23	-0.73	-12.76	
24	218966_at	MYO5C	-2.26	7.53E-24	3.85E-21	-0.75	-12.70	15q21
25	227297_at		-7.40	6.98E-30	9.47E-27	-0.66	-12.50	
26	231767_at	HOXB4	-2.82	5.71E-26	4.14E-23	-0.69	-12.44	17q21-q22
27	210365_at	RUNX1	-2.82	3.15E-26	2.63E-23	-0.69	-12.43	21q22.3
28	203544_s_at	STAM	-2.71	8.17E-21	3.01E-18	-0.76	-12.27	10p14-p13
29	204951_at	ARHH	-3.45	6.56E-21	2.46E-18	-0.75	-12.18	4p13
30	219686_at	HSA250839	-8.03	1.88E-28	2.22E-25	-0.63	-12.09	4p16.2
31	225830_at	LOC118987	-2.60	1.84E-25	1.18E-22	-0.67	-12.08	10q26.12
32	214452_at	BCAT1	-3.44	3.13E-24	1.72E-21	-0.68	-12.06	12pter-q12
33	210665_at	TFPI	-7.72	9.83E-27	9.61E-24	-0.65	-12.05	2q31-q32.1
34	226342_at		-4.92	1.60E-26	1.38E-23	-0.65	-11.99	
35	210664_s_at	TFPI	-5.36	2.36E-25	1.48E-22	-0.66	-11.97	2q31-q32.1
36	224049_at	KCNK17	-2.56	3.04E-23	1.45E-20	-0.68	-11.94	6p21.1
37	233849_s_at	ARHGAP5	-5.66	1.09E-22	4.73E-20	-0.69	-11.94	14q12
38	218086_at	NPDC1	-8.68	9.99E-28	1.07E-24	-0.63	-11.91	9q34.3
39	236198_at		-5.20	9.58E-25	5.53E-22	-0.66	-11.88	
40	210993_s_at	MADH1	-5.91	8.72E-27	8.92E-24	-0.63	-11.87	4q28

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
41	225653_at		-1.64	8.12E-20	2.43E-17	-0.73	-11.80	
42	219789_at	NPR3	-4.81	7.42E-26	5.22E-23	-0.64	-11.79	5p14-p13
43	201242_s_at	ATP1B1	-3.88	2.88E-21	1.16E-18	-0.70	-11.77	1q22-q25
44	227461_at	STN2	-3.66	1.30E-26	1.17E-23	-0.62	-11.74	14q31.1
45	209676_at	TFPI	-2.71	7.93E-23	3.64E-20	-0.66	-11.66	2q31-q32.1
46	232424_at	PRDM16	-11.32	1.11E-26	1.04E-23	-0.61	-11.64	1p36.23-p33
47	242051_at		-2.98	1.06E-22	4.69E-20	-0.66	-11.62	
48	207850_at	CXCL3	-7.78	3.83E-26	3.05E-23	-0.60	-11.50	4q21
49	220104_at	ZAP	-2.44	2.12E-20	6.92E-18	-0.68	-11.48	7q34
50	228904_at		-7.28	8.27E-24	4.08E-21	-0.62	-11.40	
1.2	**AML_inv(16) versus rest**							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	202370_s_at	CBFB	-2.73	1.66E-37	2.53E-34	-1.26	-21.16	16q22.1
2	214651_s_at	HOXA9	-12.49	1.66E-59	2.15E-55	-1.07	-20.28	7p15-p14
3	235753_at		-7.75	1.54E-59	2.15E-55	-1.03	-19.74	
4	227567_at		-4.30	1.26E-28	5.94E-26	-1.23	-19.20	
5	209905_at	HOXA9	-34.32	1.08E-55	9.27E-52	-0.99	-18.88	7p15-p14
6	226352_at		-5.62	1.31E-42	3.77E-39	-1.01	-18.21	
7	225055_at	DKFZp667M2411	-4.15	8.66E-28	3.39E-25	-1.14	-18.05	17q11.2
8	213737_x_at		-2.42	4.59E-29	2.24E-26	-1.05	-17.21	
9	217963_s_at	NGFRAP1	-12.15	1.15E-44	4.97E-41	-0.92	-17.19	Xq22.1
10	206847_s_at	HOXA7	-4.54	2.75E-38	4.45E-35	-0.96	-17.17	7p15-p14
11	201669_s_at	MARCKS	-11.36	1.99E-48	1.28E-44	-0.89	-17.12	6q22.2
12	211031_s_at	CYLN2	-6.79	1.52E-46	7.86E-43	-0.89	-16.90	7q11.23
13	222786_at	C4S-2	-3.20	1.60E-39	2.95E-36	-0.91	-16.67	7p22
14	225102_at	LOC152009	-4.28	5.55E-32	3.88E-29	-0.96	-16.48	3q21.3
15	200985_s_at	CD59	-7.51	2.08E-40	4.15E-37	-0.88	-16.36	11p13
16	219218_at	FLJ23058	-5.92	6.95E-43	2.57E-39	-0.86	-16.24	17q25.3
17	223044_at	SLC11A3	-8.62	4.64E-39	8.01E-36	-0.87	-16.11	2q32
18	228497_at	FLIPT1	-4.83	1.23E-42	3.77E-39	-0.85	-16.09	1p13.1
19	229215_at	ASCL2	-6.36	8.86E-37	1.21E-33	-0.87	-15.88	11p15.5
20	223471_at	RAB3IP	-3.25	1.08E-23	2.90E-21	-1.01	-15.69	
21	200984_s_at	CD59	-3.54	1.16E-33	1.00E-30	-0.87	-15.61	11p13
22	224952_at	DKFZP564D166	-3.75	1.29E-21	2.91E-19	-1.05	-15.56	17q23.3
23	212463_at		-5.47	6.40E-41	1.50E-37	-0.82	-15.55	
24	235521_at	HOXA3	-12.22	9.95E-42	2.57E-38	-0.81	-15.45	7p15-p14
25	230894_s_at		-9.55	2.27E-37	3.26E-34	-0.83	-15.39	
26	241706_at	LOC144402	-5.18	3.88E-31	2.42E-28	-0.88	-15.37	12q11
27	209406_at	BAG2	-3.98	8.55E-36	1.05E-32	-0.83	-15.27	6p12.3-p11.2
28	218414_s_at	NUDE1	-2.15	1.29E-23	3.39E-21	-0.97	-15.26	16p13.11
29	235391_at	LOC137392	-8.29	7.73E-41	1.67E-37	-0.80	-15.23	8q21.3
30	241985_at	FLJ37870	-5.43	1.28E-30	7.38E-28	-0.87	-15.18	5q13.3
31	213779_at	LOC129080	-2.98	1.40E-28	6.36E-26	-0.89	-15.15	22q12.1

32	213002_at	MARCKS	-3.15	1.99E-36	2.57E-33	-0.79	-14.71	6q22.2
33	216920_s_at	TRGV9	-4.15	2.34E-30	1.31E-27	-0.81	-14.39	7p15
34	204198_s_at	RUNX3	-4.72	6.51E-28	2.67E-25	-0.83	-14.39	1p36
35	218477_at	PTD011	-2.79	8.31E-25	2.53E-22	-0.85	-14.19	6p12.1
36	213241_at		-4.10	2.66E-35	2.87E-32	-0.75	-14.18	
37	213908_at		-5.71	2.97E-35	3.07E-32	-0.75	-14.14	
38	204160_s_at	ENPP4	-7.08	4.35E-34	3.89E-31	-0.75	-14.03	6p12.3
39	218332_at	BEX1	-13.66	1.78E-35	2.00E-32	-0.74	-13.95	Xq21-q23
40	226817_at		-5.11	1.17E-35	1.38E-32	-0.73	-13.93	
41	200983_x_at	CD59	-6.09	4.37E-34	3.89E-31	-0.74	-13.90	11p13
42	204197_s_at	RUNX3	-3.16	8.73E-31	5.25E-28	-0.76	-13.90	1p36
43	215806_x_at	TRGC2	-3.90	2.61E-28	1.11E-25	-0.78	-13.88	7p15
44	228365_at	LOC144402	-7.22	2.47E-26	8.63E-24	-0.80	-13.87	12q11
45	226134_s_at		-4.73	1.09E-30	6.44E-28	-0.76	-13.82	
46	218927_s_at	C4S-2	-5.27	3.52E-29	1.75E-26	-0.77	-13.75	7p22
47	211144_x_at	TRG	-4.08	2.36E-31	1.53E-28	-0.75	-13.73	7p15-p14
48	218445_at	H2AFY2	-3.99	1.27E-33	1.06E-30	-0.73	-13.71	10q22
49	210425_x_at	GOLGIN-67	-3.59	3.71E-32	2.74E-29	-0.73	-13.67	15q11.2
50	201670_s_at	MARCKS	-12.60	1.52E-34	1.51E-31	-0.71	-13.65	6q22.2
1.3	**AML_other versus rest**							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205601_s_at	HOXB5	2.85	5.38E-40	8.87E-36	0.84	15.42	17q21.3
2	231767_at	HOXB4	2.95	6.23E-39	3.45E-35	0.78	14.84	17q21-q22
3	228345_at		2.59	6.28E-39	3.45E-35	0.78	14.83	
4	205600_x_at	HOXB5	2.09	2.35E-38	9.69E-35	0.77	14.65	17q21.3
5	228904_at		7.88	1.41E-35	3.86E-32	0.79	14.34	
6	205366_s_at	HOXB6	15.60	3.43E-35	8.08E-32	0.78	14.19	17q21.3
7	205453_at	HOXB2	4.24	4.81E-36	1.58E-32	0.74	14.11	17q21-q22
8	239791_at		11.37	1.43E-32	2.94E-29	0.77	13.58	
9	236892_s_at		12.96	3.37E-32	6.17E-29	0.77	13.49	
10	238498_at		3.23	2.13E-30	3.50E-27	0.66	12.59	
11	201427_s_at	SEPP1	5.42	4.25E-30	6.37E-27	0.66	12.56	5q31
12	230743_at		2.04	1.18E-27	1.62E-24	0.65	12.03	
13	206478_at	KIAA0125	4.94	2.12E-27	2.33E-24	0.65	11.99	14q32.33
14	232424_at	PRDM16	10.87	7.67E-27	6.65E-24	0.69	11.99	1p36.23-p33
15	213940_s_at	FNBP1	1.71	1.34E-27	1.69E-24	0.63	11.94	9q34
16	204761_at	RNTRE	1.97	9.71E-27	7.69E-24	0.64	11.88	10p13
17	220377_at	C14orf110	8.83	3.75E-27	3.86E-24	0.63	11.86	14q32.33
18	212463_at		2.99	1.92E-27	2.26E-24	0.62	11.82	
19	200985_s_at	CD59	3.01	4.85E-27	4.66E-24	0.61	11.71	11p13
20	240180_at		2.07	5.09E-27	4.66E-24	0.61	11.70	
21	243010_at	MSI2	2.42	9.80E-27	7.69E-24	0.61	11.67	17q23.1
22	204030_s_at	SCHIP1	4.57	3.59E-26	2.68E-23	0.62	11.61	3q25.33

			fc	p	q	stn	t	Map Location
23	218331_s_at	FLJ20360	1.72	7.73E-26	5.53E-23	0.61	11.53	10p15.1
24	233955_x_at	HSPC195	2.19	2.58E-25	1.57E-22	0.61	11.43	5q31.3
25	212274_at	LPIN1	2.33	9.47E-26	6.50E-23	0.60	11.40	2p25.1
26	200984_s_at	CD59	2.24	1.20E-25	7.89E-23	0.60	11.35	11p13
27	228046_at	LOC152485	2.41	2.03E-25	1.29E-22	0.59	11.25	4q31.1
28	230006_s_at	DKFZp313A2432	2.04	3.16E-25	1.86E-22	0.59	11.22	11p14.2
29	225240_s_at		2.72	1.15E-24	6.53E-22	0.58	11.05	
30	226134_s_at		2.83	2.06E-24	1.13E-21	0.57	10.98	
31	236451_at		3.03	1.16E-23	6.16E-21	0.58	10.85	
32	225314_at	MGC45416	1.75	1.95E-23	1.01E-20	0.58	10.84	4p11
33	229194_at		1.86	5.69E-23	2.53E-20	0.57	10.71	
34	230285_at	DKFZp313A2432	1.96	2.11E-23	1.05E-20	0.56	10.70	11p14.2
35	230005_at	DKFZp313A2432	2.15	2.74E-23	1.33E-20	0.56	10.70	11p14.2
36	235391_at	LOC137392	3.26	2.91E-23	1.37E-20	0.56	10.67	8q21.3
37	219651_at	FLJ10713	3.60	7.26E-23	3.07E-20	0.57	10.63	3q13.13
38	203351_s_at	ORC4L	1.69	6.11E-23	2.65E-20	0.56	10.62	2q22-q23
39	230894_s_at		3.16	5.03E-23	2.30E-20	0.56	10.62	
40	204779_s_at	HOXB7	3.70	2.56E-22	1.00E-19	0.57	10.52	17q21.3
41	211709_s_at	SCGF	-1.96	1.24E-20	2.95E-18	-0.61	-10.51	19q13.3
42	201352_at	YME1L1	1.40	1.49E-21	4.63E-19	0.58	10.50	10p14
43	237591_at		2.40	1.33E-22	5.48E-20	0.55	10.49	
44	225971_at		1.75	4.80E-22	1.65E-19	0.56	10.48	
45	225811_at		1.64	3.05E-22	1.14E-19	0.55	10.46	
46	217975_at	LOC51186	2.97	2.86E-22	1.10E-19	0.55	10.45	Xq22.1
47	202076_at	BIRC2	1.48	1.69E-21	5.16E-19	0.57	10.43	11q22
48	223298_s_at	NT5C3	1.61	2.14E-22	8.61E-20	0.54	10.41	7p14.3
49	218711_s_at	SDPR	2.42	6.20E-22	2.04E-19	0.56	10.40	2q32-q33
50	228174_at		1.77	4.04E-22	1.48E-19	0.55	10.38	
1.4	**AML_t(15;17) versus rest**							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	209732_at	CLECSF2	-26.40	1.36E-101	2.54E-97	-1.58	-30.31	12p13-p12
2	204425_at	ARHGAP4	-17.17	1.85E-93	1.73E-89	-1.58	-29.87	Xq28
3	211990_at	HLA-DPA1	-9.46	1.12E-60	2.32E-57	-1.52	-27.25	6p21.3
4	205771_s_at	AKAP7	-10.46	1.36E-66	4.23E-63	-1.37	-25.29	6q23
5	213587_s_at	LOC155066	-5.57	2.68E-71	9.97E-68	-1.34	-25.10	7q36.1
6	213147_at	HOXA10	-14.24	7.73E-78	4.80E-74	-1.29	-24.67	7p15-p14
7	214651_s_at	HOXA9	-132.83	4.27E-75	1.99E-71	-1.27	-23.85	7p15-p14
8	201923_at	PRDX4	-6.33	5.98E-36	1.39E-33	-1.39	-22.94	Xp22.13
9	204362_at	SCAP2	-12.98	2.57E-60	3.99E-57	-1.24	-22.93	7p21-p15
10	241742_at	PRAM-1	-6.67	2.90E-53	2.71E-50	-1.19	-21.78	19p13.2
11	217848_s_at	PP	-4.10	2.52E-25	2.14E-23	-1.46	-21.44	10q11.1-q24
12	201137_s_at	HLA-DPB1	-9.10	1.62E-60	3.03E-57	-1.13	-21.27	6p21.3
13	225639_at	SCAP2	-10.55	2.94E-40	9.79E-38	-1.18	-20.51	7p21-p15

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
14	213150_at	HOXA10	-26.85	1.81E-62	4.83E-59	-1.07	-20.49	7p15-p14
15	201719_s_at	EPB41L2	-11.67	1.98E-60	3.36E-57	-1.07	-20.41	6q23
16	235753_at		-9.10	6.85E-62	1.59E-58	-1.06	-20.33	
17	204563_at	SELL	-5.92	5.33E-39	1.71E-36	-1.17	-20.22	1q23-q25
18	227598_at	LOC113763	-4.28	8.74E-35	1.87E-32	-1.19	-20.09	7q35
19	211991_s_at	HLA-DPA1	-13.72	1.57E-57	1.95E-54	-1.05	-19.93	6p21.3
20	216899_s_at	SCAP2	-6.03	1.14E-42	4.73E-40	-1.11	-19.79	7p21-p15
21	205453_at	HOXB2	-13.36	1.24E-59	1.78E-56	-1.03	-19.77	17q21-q22
22	210145_at	PLA2G4A	-6.78	1.02E-49	6.79E-47	-1.07	-19.68	1q25
23	200931_s_at	VCL	-3.83	3.05E-28	3.47E-26	-1.24	-19.64	10q22.1-q23
24	209905_at	HOXA9	-346.82	3.32E-58	4.41E-55	-1.05	-19.63	7p15-p14
25	201669_s_at	MARCKS	-32.71	2.33E-56	2.71E-53	-1.01	-19.13	6q22.2
26	232617_at	CTSS	-4.98	1.94E-50	1.44E-47	-1.02	-19.07	1q21
27	204361_s_at	SCAP2	-9.09	2.74E-37	7.40E-35	-1.10	-19.07	7p21-p15
28	229041_s_at		-22.54	6.79E-56	7.44E-53	-0.99	-18.91	
29	217478_s_at	HLA-DMA	-4.99	3.25E-31	5.05E-29	-1.13	-18.77	6p21.3
30	209448_at	HTATIP2	-6.86	3.17E-48	1.74E-45	-1.01	-18.75	11p15.1
31	225386_s_at	LOC92906	-19.54	6.16E-55	6.37E-52	-0.97	-18.64	2p22.2
32	206847_s_at	HOXA7	-6.01	6.99E-39	2.13E-36	-1.04	-18.44	7p15-p14
33	201753_s_at	ADD3	-5.52	4.99E-31	7.62E-29	-1.10	-18.37	10q24.2-q24.3
34	204069_at	MEIS1	-13.69	8.96E-54	8.79E-51	-0.96	-18.37	2p14-p13
35	236554_x_at	EVER2	-3.62	2.36E-22	1.44E-20	-1.25	-18.34	17q25.3
36	227353_at	EVER2	-3.75	3.33E-20	1.65E-18	-1.31	-18.18	17q25.3
37	226106_at	ZFP26	-4.43	2.85E-36	6.90E-34	-1.03	-18.04	11p15.3
38	210538_s_at	BIRC3	-7.15	8.57E-51	6.94E-48	-0.95	-18.04	11q22
39	204661_at	CDW52	-14.47	1.17E-48	6.81E-46	-0.96	-18.01	1p36
40	243618_s_at	LOC152485	-8.78	2.43E-50	1.74E-47	-0.95	-17.96	4q31.1
41	228113_at	STAT3	-4.02	1.53E-24	1.19E-22	-1.16	-17.94	17q21
42	203948_s_at	MPO	3.47	7.23E-16	2.26E-14	1.64	17.93	17q23.1
43	213844_at	HOXA5	-20.24	5.56E-52	4.93E-49	-0.94	-17.93	7p15-p14
44	34210_at	CDW52	-18.27	3.73E-50	2.58E-47	-0.95	-17.92	1p36
45	238949_at	FLJ31951	-7.52	1.42E-36	3.57E-34	-1.02	-17.91	5q33.3
46	214797_s_at	PCTK3	-4.68	2.94E-23	1.98E-21	-1.18	-17.88	1q31-q32
47	236322_at		-5.82	1.30E-26	1.27E-24	-1.11	-17.84	
48	207375_s_at	IL15RA	-4.55	1.78E-25	1.55E-23	-1.13	-17.83	10p15-p14
49	223280_x_at	MS4A6A	-13.18	3.92E-51	3.32E-48	-0.93	-17.72	11q12.1
50	228046_at	LOC152485	-4.67	1.20E-49	7.70E-47	-0.93	-17.72	4q31.1
1.5	AML_t(8;21) versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214651_s_at	HOXA9	-117.80	9.99E-76	2.72E-71	-1.29	-24.11	7p15-p14
2	213147_at	HOXA10	-10.35	8.18E-68	1.11E-63	-1.22	-23.07	7p15-p14
3	221581_s_at	WBSCR5	-6.39	7.66E-55	2.61E-51	-1.17	-21.49	7q11.23
4	213150_at	HOXA10	-35.06	4.08E-64	3.71E-60	-1.11	-21.03	7p15-p14

5	225615_at	LOC126917	-6.25	4.82E-53	1.31E-49	-1.14	-20.90	1p36.13	
6	205453_at	HOXB2	-18.06	5.86E-63	4.00E-59	-1.08	-20.62	17q21-q22	
7	235753_at		-8.61	2.64E-61	1.44E-57	-1.05	-20.18		
8	209905_at	HOXA9	-335.92	1.35E-58	6.13E-55	-1.07	-19.79	7p15-p14	
9	217963_s_at	NGFRAP1	-18.30	2.29E-58	8.93E-55	-1.02	-19.46	Xq22.1	
10	206847_s_at	HOXA7	-4.99	1.46E-49	3.31E-46	-1.02	-18.94	7p15-p14	
11	215087_at		-3.55	3.44E-47	6.26E-44	-1.01	-18.60		
12	204069_at	MEIS1	-13.25	5.13E-54	1.55E-50	-0.97	-18.48	2p14-p13	
13	226865_at		-6.07	4.27E-51	1.06E-47	-0.94	-17.95		
14	228365_at	LOC144402	-7.20	3.05E-49	5.93E-46	-0.91	-17.34	12q11	
15	213844_at	HOXA5	-13.22	1.97E-49	4.14E-46	-0.90	-17.31	7p15-p14	
16	204494_s_at	DKFZP434H132	-3.04	1.36E-35	1.20E-32	-0.97	-17.08	15q22.33	
17	204495_s_at	DKFZP434H132	-3.13	5.11E-40	6.63E-37	-0.92	-16.84	15q22.33	
18	224764_at	ARHGAP10	-6.04	5.04E-44	7.24E-41	-0.89	-16.75		10
19	206310_at	SPINK2	-54.48	1.88E-46	3.20E-43	-0.89	-16.75	4q12	
20	208890_s_at	PLXNB2	-3.85	2.27E-30	1.17E-27	-0.98	-16.57	22q13.33	
21	208091_s_at	DKFZP564K0822	-5.57	6.04E-35	4.99E-32	-0.93	-16.48	7p14.1	
22	235521_at	HOXA3	-16.47	3.71E-44	5.61E-41	-0.85	-16.14	7p15-p14	
23	208146_s_at	CPVL	-13.27	3.17E-44	5.08E-41	-0.84	-16.05	7p15-p14	
24	203017_s_at	SSX2IP	-3.72	8.29E-32	5.02E-29	-0.92	-16.02		
25	238077_at	MGC27385	-3.38	5.93E-29	2.53E-26	-0.95	-16.01	3p21.1	
26	241370_at		-2.80	6.73E-34	4.83E-31	-0.90	-15.91		
27	233955_x_at	HSPC195	-3.10	1.93E-32	1.28E-29	-0.90	-15.77	5q31.3	
28	238455_at		-4.13	1.58E-39	1.95E-36	-0.85	-15.77		
29	243806_at		-3.96	8.04E-37	8.43E-34	-0.85	-15.58		
30	224516_s_at	HSPC195	-3.29	2.11E-37	2.40E-34	-0.84	-15.50	5q31.3	
31	241706_at	LOC144402	-5.19	6.50E-32	4.03E-29	-0.88	-15.50	12q11	
32	227995_at		-7.48	5.22E-41	7.11E-38	-0.80	-15.29		
33	227853_at		-2.89	1.04E-21	2.15E-19	-0.99	-15.05		
34	224049_at	KCNK17	-2.88	1.26E-35	1.14E-32	-0.80	-14.88	6p21.1	
35	203680_at	PRKAR2B	-5.14	3.63E-36	3.54E-33	-0.80	-14.87	7q22-q31.1	
36	222996_s_at	HSPC195	-2.53	2.65E-32	1.72E-29	-0.83	-14.87	5q31.3	
37	203741_s_at	ADCY7	-4.42	2.20E-29	9.68E-27	-0.84	-14.73	16q12-q13	
38	238756_at		-3.59	4.20E-33	2.87E-30	-0.81	-14.72		
39	204030_s_at	SCHIP1	-13.47	6.50E-38	7.70E-35	-0.76	-14.53	3q25.33	
40	217975_at	LOC51186	-6.54	9.30E-32	5.51E-29	-0.81	-14.53	Xq22.1	
41	230894_s_at		-6.50	9.39E-35	7.53E-32	-0.78	-14.52		
42	213908_at		-5.92	3.53E-37	3.85E-34	-0.76	-14.50		
43	209500_x_at	TNFSF13	-3.21	8.08E-26	2.94E-23	-0.86	-14.49	17p13.1	
44	236297_at		-3.29	1.96E-33	1.37E-30	-0.78	-14.42		
45	202510_s_at	TNFAIP2	-2.96	2.59E-30	1.31E-27	-0.79	-14.17	14q32	
46	228904_at		-9.04	2.64E-36	2.66E-33	-0.74	-14.14		
47	226134_s_at		-4.30	5.65E-34	4.16E-31	-0.76	-14.11		
48	240572_s_at		-3.48	5.64E-25	1.79E-22	-0.84	-14.03		
49	229971_at	GPR114	-5.95	3.08E-28	1.20E-25	-0.80	-14.03	16q12.2	
50	211597_s_at	HOP	-9.21	1.07E-35	1.01E-32	-0.73	-13.94	4q11-q12	

Table 2

2. All-Pairs (AP)

2.1	AML_MLL versus AML_inv(16)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213737_x_at		3.65	1.30E-18	3.71E-14	2.17	15.48	
2	214651_s_at	HOXA9	22.10	4.22E-16	6.01E-12	2.26	14.60	7p15-p14
3	200665_s_at	SPARC	-14.82	7.41E-14	3.52E-10	-2.27	-14.07	5q31.3-q32
4	200953_s_at	CCND2	-4.16	1.61E-15	1.53E-11	-1.86	-13.20	12p13
5	202746_at	ITM2A	-16.05	9.80E-13	2.15E-09	-2.15	-12.88	Xq13.3-Xq21.2
6	202747_s_at	ITM2A	-16.65	8.69E-13	2.06E-09	-2.09	-12.76	Xq13.3-Xq21.2
7	235753_at		14.15	1.49E-13	6.06E-10	1.98	12.10	
8	227567_at		5.31	5.68E-15	4.05E-11	1.66	11.93	
9	229215_at	ASCL2	11.42	2.22E-13	6.34E-10	1.73	11.48	11p15.5
10	206847_s_at	HOXA7	7.10	2.07E-13	6.34E-10	1.70	11.41	7p15-p14
11	231310_at		-4.40	2.33E-14	1.33E-10	-1.54	-11.24	
12	201497_x_at	MYH11	-27.86	4.74E-11	4.22E-08	-2.16	-11.23	16p13.13-p13.12
13	200951_s_at	CCND2	-4.96	2.30E-12	4.22E-09	-1.60	-10.90	12p13
14	209905_at	HOXA9	70.38	2.46E-12	4.22E-09	1.82	10.90	7p15-p14
15	224049_at	KCNK17	-4.35	2.74E-11	2.70E-08	-1.66	-10.60	6p21.1
16	213147_at	HOXA10	5.72	2.97E-13	7.68E-10	1.48	10.56	7p15-p14
17	203949_at	MPO	-3.36	1.91E-13	6.34E-10	-1.41	-10.32	17q23.1
18	213908_at		15.52	8.76E-12	9.99E-09	1.66	10.30	
19	201496_x_at	MYH11	-6.20	5.40E-11	4.67E-08	-1.56	-10.14	16p13.13-p13.12
20	202370_s_at	CBFB	3.09	3.66E-12	5.22E-09	1.46	10.07	16q22.1
21	202931_x_at	BIN1	-3.16	1.41E-12	2.87E-09	-1.39	-10.05	2q14
22	226517_at	BCAT1	-10.55	1.85E-10	1.15E-07	-1.66	-10.05	12pter-q12
23	204082_at	PBX3	5.42	2.57E-11	2.61E-08	1.52	9.76	9q33-q34
24	212667_at	SPARC	-7.96	2.45E-10	1.42E-07	-1.54	-9.70	5q31.3-q32
25	225831_at	LOC148894	-3.79	5.89E-11	4.89E-08	-1.41	-9.59	1p36.11
26	203733_at	MYLE	3.27	3.18E-12	5.03E-09	1.30	9.50	16p13.2
27	223385_at	CYP2S1	-2.38	1.24E-10	8.39E-08	-1.38	-9.34	19q13.1
28	205330_at	MN1	-16.74	1.73E-09	5.37E-07	-1.75	-9.33	22q12.1
29	223471_at	RAB3IP	3.58	7.10E-12	8.43E-09	1.28	9.29	
30	201830_s_at	NET1	-4.44	3.73E-10	2.00E-07	-1.42	-9.26	10p15
31	202551_s_at	CRIM1	-4.62	2.91E-10	1.63E-07	-1.39	-9.23	2p21
32	210139_s_at	PMP22	-9.69	1.47E-09	4.81E-07	-1.55	-9.18	17p12-p11.2
33	224772_at	NAV1	-2.82	3.27E-10	1.79E-07	-1.37	-9.12	
34	211012_s_at	PML	-2.69	1.13E-11	1.24E-08	-1.24	-9.09	15q22
35	228058_at	LOC124220	-5.16	4.73E-12	6.12E-09	-1.22	-9.09	16p13.3
36	223299_at	LOC90701	2.79	4.18E-12	5.67E-09	1.20	9.00	18q21.31
37	214452_at	BCAT1	-4.30	3.97E-10	2.02E-07	-1.34	-8.99	12pter-q12
38	228497_at	FLIPT1	7.80	2.17E-10	1.29E-07	1.41	8.98	1p13.1
39	225102_at	LOC152009	5.25	8.41E-11	6.48E-08	1.30	8.95	3q21.3
40	201828_x_at	CXX1	2.85	2.52E-12	4.22E-09	1.17	8.91	Xq26

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
41	203948_s_at	MPO	-3.51	6.09E-12	7.55E-09	-1.19	-8.91	17q23.1
42	200602_at	APP	-6.96	1.09E-10	7.70E-08	-1.26	-8.90	21q21.3
43	218041_x_at	SLC38A2	-1.65	3.59E-12	5.22E-09	-1.17	-8.90	12q
44	225285_at		-9.24	1.04E-09	3.97E-07	-1.35	-8.82	
45	203373_at	SOCS2	13.18	2.48E-10	1.42E-07	1.34	8.82	12q
46	201029_s_at	CD99	-1.85	1.78E-11	1.88E-08	-1.18	-8.75	Xp22.32
47	213150_at	HOXA10	8.63	1.06E-10	7.70E-08	1.25	8.74	7p15-p14
48	228496_s_at	CRIM1	-2.68	8.74E-11	6.56E-08	-1.20	-8.70	2p21
49	221581_s_at	WBSCR5	2.78	3.22E-11	3.06E-08	1.19	8.70	7q11.23
50	205453_at	HOXB2	-6.83	3.79E-10	2.00E-07	-1.25	-8.69	17q21-q22

2.2 AML_MLL versus AML_other

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205453_at	HOXB2	-9.31	7.37E-41	1.53E-36	-1.03	-17.17	17q21-q22
2	211137_s_at	ATP2C1	-2.28	1.17E-37	1.22E-33	-0.93	-15.61	3q21-q24
3	226517_at	BCAT1	-7.83	7.58E-37	5.26E-33	-0.86	-14.73	12pter-q12
4	205601_s_at	HOXB5	-2.90	6.38E-36	2.66E-32	-0.85	-14.55	17q21.3
5	225344_at	ERAP140	-3.75	1.78E-34	6.17E-31	-0.86	-14.47	6q22.33
6	213258_at		-8.62	5.42E-36	2.66E-32	-0.84	-14.41	
7	231767_at	HOXB4	-3.26	3.47E-32	1.03E-28	-0.85	-14.19	17q21-q22
8	220306_at	FLJ20202	-3.44	5.04E-27	6.17E-24	-0.86	-13.62	1p11.1
9	213549_at	PRO2730	-3.10	1.32E-28	2.50E-25	-0.78	-13.05	3p21.31
10	205624_at	CPA3	-10.08	1.16E-30	3.01E-27	-0.76	-12.98	3q21-q25
11	208116_s_at	MAN1A1	-3.53	1.67E-27	2.48E-24	-0.79	-12.97	6q22
12	201830_s_at	NET1	-3.40	3.82E-27	4.97E-24	-0.79	-12.96	10p15
13	228904_at		-8.90	5.57E-29	1.16E-25	-0.76	-12.83	
14	200923_at	LGALS3BP	-7.70	5.74E-30	1.33E-26	-0.74	-12.75	17q25
15	239791_at		-10.90	1.68E-28	2.91E-25	-0.72	-12.42	
16	225532_at	LOC91768	-2.89	2.04E-26	2.12E-23	-0.74	-12.30	18q11.1
17	202746_at	ITM2A	-6.04	1.03E-26	1.20E-23	-0.73	-12.27	Xq13.3-Xq21.2
18	232424_at	PRDM16	-13.95	1.02E-27	1.64E-24	-0.73	-12.24	1p36.23-p33
19	219188_s_at	LRP16	-3.45	1.91E-25	1.65E-22	-0.74	-12.23	11q11
20	204951_at	ARHH	-3.67	9.87E-23	4.89E-20	-0.78	-12.21	4p13
21	222996_s_at	HSPC195	-2.75	7.57E-21	2.61E-18	-0.81	-12.12	5q31.3
22	225285_at		-6.47	3.28E-24	2.28E-21	-0.75	-12.10	
23	203544_s_at	STAM	-2.82	4.07E-22	1.80E-19	-0.78	-12.09	10p14-p13
24	236892_s_at		-9.76	2.76E-27	3.83E-24	-0.70	-12.06	
25	233849_s_at	ARHGAP5	-6.12	3.64E-24	2.44E-21	-0.74	-12.00	14q12
26	210365_at	RUNX1	-2.93	1.34E-25	1.21E-22	-0.71	-11.96	21q22.3
27	201829_at	NET1	-2.28	1.30E-23	8.21E-21	-0.73	-11.90	10p15
28	218086_at	NPDC1	-10.22	1.57E-26	1.72E-23	-0.70	-11.87	9q34.3
29	205383_s_at	ZNF288	-1.79	6.42E-23	3.43E-20	-0.74	-11.86	3q13.2
30	210665_at	TFPI	-8.59	2.51E-26	2.49E-23	-0.69	-11.86	2q31-q32.1
31	233955_x_at	HSPC195	-3.21	2.97E-18	6.58E-16	-0.84	-11.78	5q31.3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
32	221760_at	MAN1A1	-4.53	7.78E-26	7.36E-23	-0.69	-11.77	6q22
33	224516_s_at	HSPC195	-3.48	4.97E-20	1.54E-17	-0.78	-11.71	5q31.3
34	210664_s_at	TFPI	-5.81	3.07E-25	2.56E-22	-0.69	-11.71	2q31-q32.1
35	225830_at	LOC118987	-2.66	1.13E-24	8.74E-22	-0.70	-11.69	10q26.12
36	236513_at		-2.47	3.75E-23	2.23E-20	-0.71	-11.63	
37	201242_s_at	ATP1B1	-4.00	1.13E-21	4.70E-19	-0.73	-11.51	1q22-q25
38	202747_s_at	ITM2A	-5.98	4.68E-23	2.70E-20	-0.70	-11.50	Xq13.3-Xq21.2
39	225974_at	DKFZp762C1112	-4.47	2.86E-20	9.43E-18	-0.75	-11.47	8q21.3
40	236198_at		-5.64	2.45E-24	1.82E-21	-0.68	-11.45	
41	214390_s_at	BCAT1	-5.79	2.66E-24	1.91E-21	-0.67	-11.40	12pter-q12
42	219094_at	HSPC056	-2.19	4.62E-20	1.46E-17	-0.74	-11.39	3q22.3
43	209676_at	TFPI	-2.75	1.71E-22	8.29E-20	-0.70	-11.38	2q31-q32.1
44	210993_s_at	MADH1	-6.54	5.91E-25	4.73E-22	-0.66	-11.37	4q28
45	222920_s_at	KIAA0748	-4.00	4.38E-20	1.40E-17	-0.73	-11.30	12q13.13
46	218966_at	MYO5C	-2.19	2.75E-21	1.06E-18	-0.71	-11.29	15q21
47	231431_s_at		-1.77	2.49E-21	9.98E-19	-0.71	-11.28	
48	225831_at	LOC148894	-2.75	5.55E-20	1.67E-17	-0.72	-11.22	1p36.11
49	213158_at		-2.51	3.29E-21	1.22E-18	-0.70	-11.20	
50	236251_at		-3.62	8.24E-22	3.50E-19	-0.69	-11.20	
2.3	AML_MLL versus AML_t(15;17)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	221004_s_at	ITM2C	-9.69	6.96E-15	2.78E-11	-2.63	-16.45	2q37
2	38487_at	STAB1	-16.22	3.38E-13	4.51E-10	-2.90	-16.13	3p21.31
3	203948_s_at	MPO	-6.32	8.76E-21	2.10E-16	-2.19	-15.83	17q23.1
4	214651_s_at	HOXA9	237.17	2.30E-16	1.84E-12	2.66	15.41	7p15-p14
5	205624_at	CPA3	-36.02	6.17E-12	3.79E-09	-3.01	-14.75	3q21-q25
6	212953_x_at	CALR	-3.21	2.50E-14	6.66E-11	-2.22	-14.41	19p13.3-p13.2
7	214450_at	CTSW	-6.11	7.04E-14	1.41E-10	-2.21	-14.15	11q13.1
8	203949_at	MPO	-4.43	9.42E-19	1.13E-14	-1.91	-13.87	17q23.1
9	200953_s_at	CCND2	-6.10	3.06E-12	2.45E-09	-2.26	-13.42	12p13
10	213147_at	HOXA10	23.93	1.62E-14	4.85E-11	2.12	13.06	7p15-p14
11	238022_at		-5.73	4.14E-12	3.00E-09	-1.96	-12.30	
12	235753_at		16.83	1.12E-13	1.79E-10	2.04	12.26	
13	233072_at	KIAA1857	-11.75	7.57E-11	2.44E-08	-2.24	-12.25	9q34
14	205771_s_at	AKAP7	10.25	3.35E-14	8.02E-11	1.82	12.10	6q23
15	206871_at	ELA2	-3.69	4.90E-16	2.94E-12	-1.64	-11.89	19p13.3
16	206847_s_at	HOXA7	9.48	6.90E-14	1.41E-10	1.80	11.89	7p15-p14
17	209448_at	HTATIP2	10.38	2.48E-13	3.64E-10	1.79	11.54	11p15.1
18	204150_at	STAB1	-19.25	3.63E-10	8.30E-08	-2.23	-11.50	3p21.31
19	213587_s_at	LOC155066	7.64	6.58E-13	7.88E-10	1.79	11.29	7q36.1
20	205663_at	PCBP3	-3.93	3.63E-11	1.36E-08	-1.79	-11.19	21q22.3
21	201522_x_at	SNRPN	4.63	2.51E-15	1.20E-11	1.54	11.19	15q12
22	212509_s_at		-6.33	1.53E-10	4.37E-08	-1.87	-11.08	

23	209905_at	HOXA9	720.22	1.83E-12	1.75E-09	1.92	11.06	7p15-p14
24	205349_at	GNA15	-4.14	1.47E-12	1.53E-09	-1.62	-11.03	19p13.3
25	200951_s_at	CCND2	-6.76	2.21E-10	5.88E-08	-1.88	-10.98	12p13
26	206761_at	TACTILE	-28.74	1.21E-09	2.02E-07	-2.29	-10.90	3q13.13
27	201029_s_at	CD99	-2.16	1.08E-14	3.69E-11	-1.48	-10.74	Xp22.32
28	217848_s_at	PP	3.89	1.09E-13	1.79E-10	1.49	10.59	10q11.1-q24
29	225532_at	LOC91768	-5.64	9.02E-10	1.64E-07	-1.92	-10.59	18q11.1
30	200952_s_at	CCND2	-4.07	2.77E-10	6.83E-08	-1.76	-10.57	12p13
31	204425_at	ARHGAP4	15.58	4.11E-12	3.00E-09	1.65	10.49	Xq28
32	204082_at	PBX3	8.50	2.90E-12	2.40E-09	1.61	10.47	9q33-q34
33	231736_x_at	MGST1	-2.80	2.58E-13	3.64E-10	-1.46	-10.42	12p12.3-p12.1
34	210788_s_at	retSDR4	-2.38	2.11E-11	9.75E-09	-1.57	-10.41	14q22.3
35	224918_x_at	MGST1	-2.62	9.12E-14	1.68E-10	-1.42	-10.30	12p12.3-p12.1
36	201596_x_at	KRT18	-8.14	5.16E-10	1.08E-07	-1.69	-10.20	12q13
37	213150_at	HOXA10	45.69	1.41E-11	7.20E-09	1.71	10.17	7p15-p14
38	218404_at	SNX10	6.77	5.71E-12	3.60E-09	1.53	10.09	7p15.2
39	225386_s_at	LOC92906	34.47	1.65E-11	8.20E-09	1.66	10.08	2p22.2
40	211474_s_at	SERPINB6	4.55	2.77E-12	2.40E-09	1.47	10.04	6p25
41	221253_s_at	MGC3178	-2.99	2.44E-10	6.44E-08	-1.59	-10.03	6p24.3
42	228083_at	CACNA2D4	11.77	1.68E-11	8.20E-09	1.57	9.93	12p13.33
43	213571_s_at	EIF4EL3	2.54	6.08E-13	7.67E-10	1.37	9.84	2q37.1
44	208852_s_at	CANX	-2.26	6.45E-11	2.18E-08	-1.46	-9.78	5q35
45	227999_at	LOC170394	3.11	7.06E-13	8.06E-10	1.36	9.76	10q26.3
46	217716_s_at	SEC61A1	-1.93	1.04E-11	5.68E-09	-1.40	-9.72	3q21.3
47	202265_at	BMI1	4.29	8.23E-12	4.70E-09	1.43	9.71	10p11.23
48	217853_at	TEM6	6.43	1.19E-11	6.31E-09	1.43	9.66	7p15.1
49	223663_at	FLJ37970	6.99	2.35E-12	2.17E-09	1.37	9.66	11q12.3
50	228263_at	GRASP	-2.66	3.59E-12	2.77E-09	-1.36	-9.63	12q13.13

2.4 AML_MLL versus AML_t(8;21)

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214651_s_at	HOXA9	207.35	2.33E-16	6.38E-12	2.65	15.40	7p15-p14
2	221581_s_at	WBSCR5	10.61	3.46E-15	2.36E-11	2.04	13.41	7q11.23
3	213147_at	HOXA10	17.19	2.21E-14	1.01E-10	2.00	12.78	7p15-p14
4	235753_at		15.72	1.24E-13	4.83E-10	2.01	12.20	
5	201105_at	LGALS1	7.06	3.40E-15	2.36E-11	1.63	11.87	22q13.1
6	206847_s_at	HOXA7	7.80	1.77E-13	6.06E-10	1.79	11.69	7p15-p14
7	227853_at		3.59	7.38E-15	4.04E-11	1.54	11.33	
8	203949_at	MPO	-4.06	7.26E-16	9.92E-12	-1.47	-11.16	17q23.1
9	209905_at	HOXA9	687.57	1.83E-12	4.55E-09	1.92	11.06	7p15-p14
10	213908_at		16.07	8.41E-12	1.53E-08	1.68	10.33	
11	213150_at	HOXA10	58.80	1.26E-11	2.16E-08	1.73	10.23	7p15-p14
12	210314_x_at	TNFSF13	4.81	5.81E-13	1.59E-09	1.42	10.22	17p13.1
13	228827_at		-110.08	4.44E-10	2.89E-07	-1.99	-10.05	

#	affy id	HUGO name						Map Location
14	228083_at	CACNA2D4	12.77	1.51E-11	2.29E-08	1.60	10.05	12p13.33
15	209500_x_at	TNFSF13	4.18	3.77E-12	7.93E-09	1.39	9.82	17p13.1
16	204082_at	PBX3	6.63	5.42E-12	1.06E-08	1.39	9.77	9q33-q34
17	228058_at	LOC124220	-6.07	2.57E-12	5.84E-09	-1.33	-9.70	16p13.3
18	203948_s_at	MPO	-4.62	4.25E-13	1.29E-09	-1.28	-9.66	17q23.1
19	206940_s_at	POU4F1	-41.89	1.43E-09	6.02E-07	-1.86	-9.46	13q21.1-q22
20	212423_at	FLJ90798	5.26	1.45E-11	2.29E-08	1.34	9.42	10q22.3
21	201944_at	HEXB	3.49	5.23E-11	5.29E-08	1.44	9.41	5q13
22	223562_at	PARVG	3.11	2.14E-11	2.67E-08	1.34	9.35	22q13.2-q13
23	229406_at		-12.04	2.06E-09	7.54E-07	-1.65	-9.19	
24	205639_at	AOAH	5.75	2.05E-11	2.67E-08	1.29	9.18	7p14-p12
25	204202_at	KIAA1023	3.45	2.15E-11	2.67E-08	1.28	9.13	7p22.3
26	205529_s_at	CBFA2T1	-12.90	2.76E-09	8.88E-07	-1.70	-9.10	8q22
27	230650_at		-5.19	2.41E-09	8.23E-07	-1.55	-9.01	
28	206009_at	ITGA9	-3.49	2.03E-10	1.50E-07	-1.30	-8.95	3p21.3
29	203859_s_at	PALM	-5.31	1.28E-09	5.66E-07	-1.39	-8.88	19p13.3
30	217853_at	TEM6	5.32	2.90E-11	3.44E-08	1.22	8.87	7p15.1
31	201850_at	CAPG	8.40	4.01E-10	2.67E-07	1.37	8.73	2cen-q24
32	224415_s_at	HINT2	1.98	1.84E-11	2.65E-08	1.16	8.66	9p13.1
33	216417_x_at	HOXB9	3.56	3.49E-11	3.81E-08	1.17	8.64	17q21.3
34	203733_at	MYLE	2.65	6.93E-11	6.53E-08	1.18	8.59	16p13.2
35	211341_at	POU4F1	-266.20	9.63E-09	2.23E-06	-1.69	-8.54	13q21.1-q22
36	225245_x_at	H2AFJ	4.56	3.12E-11	3.55E-08	1.15	8.54	12p12
37	204069_at	MEIS1	20.28	8.95E-10	4.51E-07	1.42	8.54	2p14-p13
38	205528_s_at	CBFA2T1	-41.63	1.17E-08	2.56E-06	-1.63	-8.45	8q22
39	206761_at	TACTILE	-19.71	1.31E-08	2.72E-06	-1.57	-8.38	3q13.13
40	204880_at	MGMT	-2.31	1.57E-10	1.26E-07	-1.14	-8.36	10q26
41	225386_s_at	LOC92906	7.38	1.95E-10	1.48E-07	1.15	8.31	2p22.2
42	225009_at	CKLFSF4	4.99	6.86E-10	3.83E-07	1.22	8.29	16q21
43	202746_at	ITM2A	-6.60	3.24E-09	9.84E-07	-1.25	-8.28	Xq13.3-Xq21.2
44	218217_at	RISC	4.76	3.65E-10	2.49E-07	1.17	8.28	17q23.1
45	232227_at		-11.48	1.52E-08	2.99E-06	-1.50	-8.27	
46	238756_at		3.91	6.11E-10	3.55E-07	1.20	8.26	
47	224301_x_at	H2AFJ	3.97	1.00E-10	8.64E-08	1.11	8.24	12p12
48	212459_x_at	SUCLG2	3.21	4.89E-11	5.14E-08	1.09	8.21	3p14.2
49	241706_at	LOC144402	6.44	1.09E-09	5.31E-07	1.19	8.13	12q11
50	225344_at	ERAP140	-4.28	9.94E-09	2.25E-06	-1.30	-8.13	6q22.33
2.5	AML_inv(16) versus AML_other							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214651_s_at	HOXA9	-13.40	4.95E-61	1.11E-56	-1.28	-21.68	7p15-p14
2	202370_s_at	CBFB	-2.80	3.77E-40	6.52E-37	-1.33	-20.73	16q22.1
3	235753_at		-8.12	2.95E-57	3.32E-53	-1.20	-20.31	
4	209905_at	HOXA9	-35.64	7.65E-54	5.74E-50	-1.15	-19.48	7p15-p14

5	217963_s_at	NGFRAP1	-14.00	6.77E-49	3.81E-45	-1.11	-18.59	Xq22.1
6	206847_s_at	HOXA7	-4.85	4.94E-41	1.11E-37	-1.12	-18.18	7p15-p14
7	226352_at		-6.13	2.96E-44	1.33E-40	-1.08	-17.90	
8	227567_at		-4.26	9.84E-30	4.52E-27	-1.21	-17.87	
9	200985_s_at	CD59	-8.70	2.16E-43	8.08E-40	-1.01	-17.01	11p13
10	225055_at	DKFZp667M2411	-4.05	1.50E-27	5.43E-25	-1.14	-16.82	17q11.2
11	222786_at	C4S-2	-3.46	8.40E-41	1.72E-37	-1.00	-16.63	7p22
12	223044_at	SLC11A3	-9.88	1.31E-41	3.68E-38	-0.99	-16.59	2q32
13	200984_s_at	CD59	-3.98	3.03E-38	3.79E-35	-1.00	-16.42	11p13
14	241706_at	LOC144402	-5.74	4.41E-35	4.96E-32	-1.02	-16.32	12q11
15	201669_s_at	MARCKS	-12.40	1.44E-42	4.62E-39	-0.96	-16.26	6q22.2
16	213737_x_at		-2.37	2.81E-28	1.11E-25	-1.06	-16.05	
17	230894_s_at		-11.09	7.85E-40	1.26E-36	-0.95	-15.93	
18	212463_at		-6.35	4.38E-41	1.10E-37	-0.94	-15.89	
19	209406_at	BAG2	-4.45	1.48E-38	2.08E-35	-0.95	-15.84	6p12.3-p11.2
20	235521_at	HOXA3	-12.50	3.47E-40	6.50E-37	-0.92	-15.66	7p15-p14
21	211031_s_at	CYLN2	-6.80	1.92E-39	2.89E-36	-0.91	-15.46	7q11.23
22	223471_at	RAB3IP	-3.34	1.52E-25	4.08E-23	-1.03	-15.27	
23	219218_at	FLJ23058	-6.36	4.03E-38	4.78E-35	-0.89	-15.13	17q25.3
24	235391_at	LOC137392	-9.68	2.69E-38	3.56E-35	-0.89	-15.12	8q21.3
25	218414_s_at	NUDE1	-2.24	3.27E-26	1.01E-23	-1.00	-15.08	16p13.11
26	225102_at	LOC152009	-4.29	1.88E-31	1.06E-28	-0.94	-15.07	3q21.3
27	241985_at	FLJ37870	-5.84	2.35E-32	1.47E-29	-0.92	-14.89	5q13.3
28	224952_at	DKFZP564D166	-3.74	2.17E-22	4.57E-20	-1.04	-14.71	17q23.3
29	228365_at	LOC144402	-8.07	6.25E-30	2.93E-27	-0.92	-14.70	12q11
30	226134_s_at		-5.47	3.32E-34	3.11E-31	-0.87	-14.55	
31	213779_at	LOC129080	-2.83	8.64E-26	2.43E-23	-0.94	-14.38	22q12.1
32	217975_at	LOC51186	-6.81	4.96E-30	2.38E-27	-0.89	-14.33	Xq22.1
33	218477_at	PTD011	-2.94	4.65E-27	1.59E-24	-0.92	-14.31	6p12.1
34	213353_at	ABCA5	-3.30	3.29E-21	6.16E-19	-1.02	-14.29	17q24.3
35	204198_s_at	RUNX3	-5.12	4.28E-30	2.14E-27	-0.88	-14.25	1p36
36	205366_s_at	HOXB6	-13.05	8.00E-35	8.57E-32	-0.84	-14.22	17q21.3
37	203949_at	MPO	2.11	6.45E-21	1.15E-18	1.02	14.20	17q23.1
38	213908_at		-5.12	6.44E-33	4.87E-30	-0.85	-14.15	
39	243010_at	MSI2	-3.27	1.27E-34	1.30E-31	-0.83	-14.14	17q23.1
40	218445_at	H2AFY2	-4.41	1.99E-34	1.95E-31	-0.83	-14.13	10q22
41	239791_at		-14.81	1.06E-33	9.56E-31	-0.83	-13.93	
42	225240_s_at		-4.72	3.99E-31	2.14E-28	-0.85	-13.92	
43	212314_at	KIAA0746	-4.14	2.35E-30	1.20E-27	-0.85	-13.92	4p15.2
44	216920_s_at	TRGV9	-4.30	4.42E-30	2.16E-27	-0.85	-13.85	7p15
45	201427_s_at	SEPP1	-10.45	1.32E-32	8.72E-30	-0.82	-13.83	5q31
46	204160_s_at	ENPP4	-8.03	2.84E-33	2.46E-30	-0.82	-13.83	6p12.3
47	213002_at	MARCKS	-3.28	5.48E-33	4.40E-30	-0.82	-13.80	6q22.2
48	205600_x_at	HOXB5	-2.32	1.33E-26	4.28E-24	-0.88	-13.80	17q21.3
49	238778_at	FLJ32798	-7.06	8.45E-33	5.94E-30	-0.82	-13.79	10p11.1
50	229215_at	ASCL2	-5.96	7.58E-31	3.97E-28	-0.83	-13.78	11p15.5

2.6	AML_inv(16) versus AML_t(15;17)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211990_at	HLA-DPA1	12.87	6.59E-19	1.76E-14	3.40	20.83	6p21.3
2	214450_at	CTSW	-7.68	6.17E-13	5.50E-10	-2.95	-15.78	11q13.1
3	204661_at	CDW52	33.90	2.84E-14	7.34E-11	2.75	15.39	1p36
4	38487_at	STAB1	-7.92	2.48E-12	1.89E-09	-3.00	-15.22	3p21.31
5	209732_at	CLECSF2	30.41	1.19E-13	1.77E-10	2.75	14.76	12p13-p12
6	217478_s_at	HLA-DMA	7.72	5.11E-15	2.13E-11	2.38	14.68	6p21.3
7	221004_s_at	ITM2C	-4.93	9.59E-14	1.51E-10	-2.43	-14.58	2q37
8	34210_at	CDW52	43.95	1.36E-13	1.92E-10	2.64	14.51	1p36
9	200654_at	P4HB	-2.26	2.17E-15	1.16E-11	-2.24	-14.34	17q25
10	203535_at	S100A9	8.87	5.77E-16	5.14E-12	2.17	14.08	1q21
11	209619_at	CD74	5.65	4.69E-17	6.26E-13	2.09	13.92	5q32
12	238022_at		-8.04	2.75E-12	2.00E-09	-2.31	-13.37	
13	200931_s_at	VCL	3.99	1.89E-15	1.16E-11	2.04	13.29	10q22.1-q23
14	201923_at	PRDX4	7.40	5.83E-14	1.11E-10	2.12	13.18	Xp22.13
15	209312_x_at	HLA-DRB1	8.91	4.83E-14	9.92E-11	2.10	13.11	6p21.3
16	208306_x_at	HLA-DRB4	9.68	8.26E-14	1.47E-10	2.12	13.11	6p21.3
17	205624_at	CPA3	-8.88	1.01E-11	5.61E-09	-2.34	-13.07	3q21-q25
18	204563_at	SELL	9.19	5.06E-13	5.01E-10	2.18	12.90	1q23-q25
19	204670_x_at	HLA-DRB5	6.82	5.58E-15	2.13E-11	1.94	12.69	6p21.3
20	231310_at		4.86	4.39E-14	9.77E-11	1.98	12.63	
21	208891_at	DUSP6	7.87	1.16E-14	3.88E-11	1.92	12.52	12q22-q23
22	212953_x_at	CALR	-2.83	3.00E-14	7.34E-11	-1.93	-12.49	19p13.3-p13.2
23	238365_s_at		-10.18	1.04E-10	3.05E-08	-2.44	-12.36	
24	207375_s_at	IL15RA	4.86	3.02E-14	7.34E-11	1.86	12.14	10p15-p14
25	221059_s_at	CHST6	6.79	8.00E-13	6.89E-10	1.98	12.11	16q22
26	208982_at	PECAM1	4.84	3.84E-13	4.22E-10	1.91	11.99	17q23
27	205718_at	ITGB7	6.51	4.60E-13	4.72E-10	1.91	11.97	12q13.13
28	205663_at	PCBP3	-4.82	1.21E-11	6.17E-09	-2.01	-11.95	21q22.3
29	229168_at	DKFZp434K0621	-6.66	3.87E-10	8.47E-08	-2.35	-11.57	5q35.3
30	233072_at	KIAA1857	-7.11	2.16E-10	5.54E-08	-2.13	-11.47	9q34
31	211991_s_at	HLA-DPA1	25.47	2.35E-11	1.07E-08	2.09	11.45	6p21.3
32	224583_at	COTL1	5.47	3.94E-13	4.22E-10	1.78	11.44	16q23.3
33	232617_at	CTSS	8.68	2.07E-11	9.71E-09	2.05	11.43	1q21
34	224839_s_at	GPT2	-8.67	4.98E-11	1.73E-08	-1.95	-11.38	16q12.1
35	201497_x_at	MYH11	29.05	4.61E-11	1.65E-08	2.19	11.25	16p13.13-p13.12
36	241742_at	PRAM-1	11.62	2.96E-11	1.22E-08	2.01	11.23	19p13.2
37	226878_at		4.23	4.00E-12	2.61E-09	1.81	11.18	
38	201137_s_at	HLA-DPB1	15.27	5.30E-11	1.81E-08	1.99	10.99	6p21.3
39	208689_s_at	RPN2	-1.74	1.74E-13	2.32E-10	-1.65	-10.96	20q12-q13.1
40	201496_x_at	MYH11	10.95	8.48E-12	5.03E-09	1.78	10.95	16p13.13-p13.12
41	202803_s_at	ITGB2	5.33	5.45E-13	5.20E-10	1.66	10.86	21q22.3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
42	204150_at	STAB1	-9.25	1.13E-09	2.11E-07	-2.20	-10.85	3p21.31
43	238376_at		3.13	1.34E-12	1.11E-09	1.68	10.82	
44	202820_at	AHR	7.11	2.91E-12	2.05E-09	1.69	10.77	7p15
45	202644_s_at	TNFAIP3	2.63	9.42E-14	1.51E-10	1.60	10.76	6q23
46	223280_x_at	MS4A6A	24.32	1.17E-10	3.37E-08	2.00	10.68	11q12.1
47	228046_at	LOC152485	3.11	5.33E-12	3.39E-09	1.69	10.68	4q31.1
48	228113_at	STAT3	3.41	2.65E-13	3.31E-10	1.60	10.63	17q21
49	213779_at	LOC129080	-6.48	1.04E-09	1.96E-07	-2.02	-10.63	22q12.1
50	210982_s_at	HLA-DRA	7.45	1.37E-12	1.11E-09	1.63	10.60	6p21.3
2.7	AML_inv(16) versus AML_t(8;21)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	207075_at	CIAS1	6.20	6.53E-13	4.40E-09	2.14	12.84	1q44
2	205718_at	ITGB7	7.97	2.06E-13	2.37E-09	1.94	12.42	12q13.13
3	208890_s_at	PLXNB2	5.47	2.82E-13	2.37E-09	1.95	12.41	22q13.33
4	224764_at	ARHGAP10	9.78	6.18E-12	1.89E-08	2.04	11.88	10
5	205419_at	EBI2	7.28	3.55E-12	1.52E-08	1.93	11.76	13q32.2
6	218795_at	ACP6	-4.43	2.56E-13	2.37E-09	-1.71	-11.41	1q21
7	224049_at	KCNK17	4.96	2.15E-11	5.57E-08	1.93	11.23	6p21.1
8	201497_x_at	MYH11	27.72	4.77E-11	7.64E-08	2.18	11.23	16p13.13-p13.12
9	218236_s_at	PRKCN	5.61	2.01E-12	1.13E-08	1.65	10.88	2p21
10	238604_at		3.46	2.13E-13	2.37E-09	1.50	10.47	
11	205453_at	HOXB2	15.78	1.65E-10	1.74E-07	1.88	10.41	17q21-q22
12	201596_x_at	KRT18	9.11	3.90E-11	6.91E-08	1.67	10.37	12q13
13	224724_at	SULF2	26.58	2.51E-10	2.26E-07	1.96	10.31	20q12-13.2
14	209365_s_at	ECM1	3.32	5.67E-12	1.89E-08	1.52	10.17	1q21
15	228827_at		-100.56	4.49E-10	3.22E-07	-1.97	-10.04	
16	201496_x_at	MYH11	6.61	2.98E-11	6.14E-08	1.55	10.02	16p13.13-p13.12
17	200665_s_at	SPARC	3.67	6.00E-12	1.89E-08	1.49	10.02	5q31.3-q32
18	201739_at	SGK	4.55	3.60E-12	1.52E-08	1.46	9.97	6q23
19	201944_at	HEXB	2.26	3.09E-11	6.14E-08	1.52	9.92	5q13
20	209500_x_at	TNFSF13	4.26	1.51E-10	1.70E-07	1.52	9.61	17p13.1
21	235359_at		3.06	5.86E-11	8.57E-08	1.46	9.56	
22	203320_at	LNK	2.89	7.98E-11	1.12E-07	1.47	9.56	12q24
23	208683_at	CAPN2	3.25	1.30E-11	3.66E-08	1.39	9.47	1q41-q42
24	211084_x_at	PRKCN	4.90	2.81E-11	6.14E-08	1.40	9.46	2p21
25	217849_s_at	CDC42BPB	5.22	3.31E-11	6.19E-08	1.41	9.46	14q32.3
26	210314_x_at	TNFSF13	5.02	1.80E-10	1.80E-07	1.48	9.45	17p13.1
27	206940_s_at	POU4F1	-37.07	1.50E-09	8.29E-07	-1.82	-9.42	13q21.1-q22
28	201887_at	IL13RA1	4.32	3.65E-10	2.73E-07	1.52	9.40	Xq24
29	223249_at	CLDN12	3.44	5.41E-11	8.27E-08	1.41	9.40	7q21
30	240572_s_at		3.50	3.10E-11	6.14E-08	1.39	9.40	
31	220974_x_at	BA108L7.2	4.98	1.02E-10	1.33E-07	1.39	9.22	10q24.31
32	205529_s_at	CBFA2T1	-14.03	2.39E-09	1.17E-06	-1.70	-9.16	8q22

33	236738_at		7.02	4.91E-10	3.38E-07	1.44	9.10	
34	201005_at	CD9	7.50	3.32E-10	2.65E-07	1.40	9.04	12p13.3
35	201360_at	CST3	4.55	3.35E-10	2.65E-07	1.39	9.02	20p11.21
36	225102_at	LOC152009	-3.87	3.38E-10	2.65E-07	-1.34	-8.83	3q21.3
37	218237_s_at	SLC38A1	3.46	4.08E-10	2.98E-07	1.35	8.82	12q12
38	205330_at	MN1	9.47	3.99E-09	1.74E-06	1.56	8.81	22q12.1
39	225602_at	C9orf19	2.74	4.53E-11	7.63E-08	1.26	8.75	9p13-p12
40	220591_s_at	FLJ22843	3.10	7.60E-10	4.74E-07	1.35	8.72	Xp11.3
41	229309_at		10.85	4.42E-09	1.91E-06	1.52	8.71	
42	229383_at		5.16	3.78E-09	1.67E-06	1.46	8.66	
43	201425_at	ALDH2	6.54	3.46E-10	2.65E-07	1.29	8.64	12q24.2
44	229406_at		-8.50	3.12E-09	1.48E-06	-1.43	-8.63	
45	208033_s_at	ATBF1	4.00	6.81E-10	4.41E-07	1.30	8.57	16q22.3-q23.1
46	205859_at	LY86	3.64	2.66E-09	1.28E-06	1.38	8.57	6p24.3
47	211341_at	POU4F1	-162.01	1.01E-08	3.29E-06	-1.68	-8.52	13q21.1-q22
48	224579_at		3.69	1.71E-09	9.28E-07	1.33	8.52	
49	202283_at	SERPINF1	8.19	2.29E-09	1.15E-06	1.35	8.51	17p13.1
50	226818_at	LOC219972	10.78	6.29E-09	2.38E-06	1.45	8.48	11q12.1
2.8	AML_other versus AML_t(15;17)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	209732_at	CLECSF2	23.83	1.34E-83	2.30E-79	1.67	28.16	12p13-p12
2	204425_at	ARHGAP4	17.18	2.20E-78	1.26E-74	1.60	26.84	Xq28
3	213147_at	HOXA10	15.20	1.90E-78	1.26E-74	1.60	26.82	7p15-p14
4	214651_s_at	HOXA9	143.81	2.25E-72	9.68E-69	1.54	25.27	7p15-p14
5	205771_s_at	AKAP7	11.13	5.36E-63	1.84E-59	1.39	23.11	6q23
6	211990_at	HLA-DPA1	9.07	1.58E-56	2.47E-53	1.41	23.06	6p21.3
7	213587_s_at	LOC155066	5.52	1.08E-62	3.09E-59	1.37	22.85	7q36.1
8	217848_s_at	PP	4.35	8.76E-29	1.28E-26	1.58	21.99	10q11.1-q24
9	205453_at	HOXB2	16.15	2.10E-61	5.15E-58	1.28	21.55	17q21-q22
10	204362_at	SCAP2	13.62	1.55E-56	2.47E-53	1.28	21.20	7p21-p15
11	235753_at		9.65	3.26E-59	7.01E-56	1.25	20.99	
12	213150_at	HOXA10	29.01	1.91E-58	3.65E-55	1.24	20.83	7p15-p14
13	201923_at	PRDX4	6.00	3.38E-35	9.53E-33	1.36	20.54	Xp22.13
14	209905_at	HOXA9	364.76	8.21E-56	1.18E-52	1.25	20.31	7p15-p14
15	241742_at	PRAM-1	6.29	1.86E-47	1.77E-44	1.23	20.07	19p13.2
16	204563_at	SELL	6.10	2.11E-40	9.81E-38	1.27	19.91	1q23-q25
17	206847_s_at	HOXA7	6.47	7.24E-42	3.66E-39	1.22	19.48	7p15-p14
18	203948_s_at	MPO	-4.21	1.64E-16	5.08E-15	-1.92	-19.25	17q23.1
19	210145_at	PLA2G4A	7.35	2.23E-49	2.74E-46	1.16	19.15	1q25
20	227598_at	LOC113763	4.41	2.11E-37	7.26E-35	1.21	18.97	7q35
21	225639_at	SCAP2	10.77	3.44E-41	1.69E-38	1.19	18.95	7p21-p15
22	200931_s_at	VCL	3.91	3.76E-31	7.02E-29	1.24	18.54	10q22.1-q23
23	216899_s_at	SCAP2	6.20	2.19E-42	1.18E-39	1.12	18.22	7p21-p15

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
24	213844_at	HOXA5	21.84	1.62E-49	2.14E-46	1.08	18.22	7p15-p14
25	203949_at	MPO	-2.78	9.96E-19	4.21E-17	-1.53	-18.19	17q23.1
26	201137_s_at	HLA-DPB1	8.40	1.15E-47	1.16E-44	1.08	18.12	6p21.3
27	207375_s_at	IL15RA	4.87	4.12E-29	6.15E-27	1.23	18.12	10p15-p14
28	228365_at	LOC144402	10.29	9.97E-49	1.14E-45	1.08	18.09	12q11
29	226106_at	ZFP26	4.87	2.33E-40	1.05E-37	1.12	18.00	11p15.3
30	227353_at	EVER2	3.86	1.83E-22	1.27E-20	1.33	17.83	17q25.3
31	201669_s_at	MARCKS	36.04	2.82E-47	2.55E-44	1.08	17.83	6q22.2
32	214797_s_at	PCTK3	4.81	6.85E-25	6.65E-23	1.27	17.82	1q31-q32
33	228046_at	LOC152485	5.35	9.71E-48	1.04E-44	1.05	17.76	4q31.1
34	236554_x_at	EVER2	3.68	3.53E-24	3.13E-22	1.27	17.70	17q25.3
35	201753_s_at	ADD3	5.76	1.09E-33	2.89E-31	1.14	17.67	10q24.2-q24.3
36	238058_at		3.60	3.52E-46	2.63E-43	1.06	17.65	
37	204361_s_at	SCAP2	9.39	2.34E-38	8.54E-36	1.10	17.64	7p21-p15
38	243618_s_at	LOC152485	9.95	9.52E-47	8.18E-44	1.04	17.50	4q31.1
39	204069_at	MEIS1	14.69	1.72E-46	1.41E-43	1.04	17.46	2p14-p13
40	201719_s_at	EPB41L2	11.86	1.96E-46	1.53E-43	1.03	17.39	6q23
41	236322_at		6.08	1.68E-29	2.58E-27	1.15	17.30	
42	226077_at	FLJ31951	5.74	1.91E-35	5.46E-33	1.08	17.11	5q33.3
43	226764_at	LOC152485	10.41	7.04E-45	5.04E-42	1.01	16.97	4q31.1
44	228113_at	STAT3	4.09	8.87E-27	1.05E-24	1.15	16.94	17q21
45	210538_s_at	BIRC3	7.92	1.20E-44	8.26E-42	1.00	16.91	11q22
46	211991_s_at	HLA-DPA1	12.30	5.71E-44	3.78E-41	1.01	16.90	6p21.3
47	241706_at	LOC144402	5.87	5.69E-36	1.69E-33	1.05	16.85	12q11
48	232617_at	CTSS	4.88	1.14E-42	6.54E-40	1.01	16.84	1q21
49	223475_at	LOC83690	12.69	8.19E-43	4.85E-40	1.00	16.77	8q13.3
50	231767_at	HOXB4	4.42	2.02E-39	8.09E-37	1.02	16.74	17q21-q22
2.9	AML_other versus AML_t(8;21)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214651_s_at	HOXA9	125.73	2.66E-72	6.74E-68	1.54	25.24	7p15-p14
2	213147_at	HOXA10	10.92	3.46E-69	4.38E-65	1.48	24.86	7p15-p14
3	205453_at	HOXB2	21.52	5.08E-63	4.29E-59	1.31	22.08	17q21-q22
4	213150_at	HOXA10	37.33	3.97E-59	2.51E-55	1.26	21.12	7p15-p14
5	235753_at		9.01	1.72E-58	8.72E-55	1.22	20.69	
6	217963_s_at	NGFRAP1	21.05	2.48E-58	1.05E-54	1.21	20.59	Xq22.1
7	209905_at	HOXA9	348.22	8.39E-56	3.03E-52	1.25	20.31	7p15-p14
8	206847_s_at	HOXA7	5.32	2.02E-51	6.38E-48	1.19	19.88	7p15-p14
9	221581_s_at	WBSCR5	6.28	4.50E-50	1.27E-46	1.19	19.75	7q11.23
10	225615_at	LOC126917	6.37	1.44E-48	3.65E-45	1.12	18.79	1p36.13
11	228365_at	LOC144402	8.05	4.42E-48	1.02E-44	1.04	17.75	12q11
12	213844_at	HOXA5	14.10	1.93E-47	4.07E-44	1.04	17.59	7p15-p14
13	204069_at	MEIS1	14.03	2.37E-46	4.62E-43	1.04	17.43	2p14-p13
14	233955_x_at	HSPC195	3.49	2.58E-38	3.27E-35	1.07	17.28	5q31.3

Table 1+2

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
15	215087_at		3.74	3.17E-44	5.74E-41	1.03	17.24	
16	226865_at		6.38	2.18E-43	3.68E-40	0.97	16.49	
17	241706_at	LOC144402	5.75	7.54E-36	6.16E-33	1.02	16.44	12q11
18	235521_at	HOXA3	16.81	5.30E-42	8.38E-39	0.98	16.30	7p15-p14
19	224516_s_at	HSPC195	3.69	2.43E-40	3.42E-37	0.97	16.18	5q31.3
20	206310_at	SPINK2	58.90	5.20E-41	7.75E-38	0.97	16.07	4q12
21	204494_s_at	DKFZP434H132	3.14	6.33E-36	5.52E-33	0.98	16.00	15q22.33
22	243806_at		4.12	1.60E-37	1.76E-34	0.97	15.95	
23	222996_s_at	HSPC195	2.81	6.32E-37	6.40E-34	0.97	15.89	5q31.3
24	204495_s_at	DKFZP434H132	3.29	1.79E-38	2.39E-35	0.95	15.80	15q22.33
25	241370_at		2.96	2.19E-35	1.59E-32	0.95	15.60	
26	203017_s_at	SSX2IP	3.99	4.05E-34	2.63E-31	0.96	15.57	
27	217975_at	LOC51186	7.57	4.68E-36	4.38E-33	0.94	15.45	Xq22.1
28	231767_at	HOXB4	3.71	1.33E-35	1.04E-32	0.94	15.43	17q21-q22
29	208091_s_at	DKFZP564K0822	5.64	7.05E-34	4.35E-31	0.94	15.35	7p14.1
30	230894_s_at		7.58	1.22E-37	1.40E-34	0.91	15.25	
31	228904_at		11.24	3.30E-38	3.98E-35	0.91	15.22	
32	208890_s_at	PLXNB2	3.78	1.39E-29	6.16E-27	0.97	15.21	22q13.33
33	238077_at	MGC27385	3.45	6.48E-30	2.93E-27	0.96	15.14	3p21.1
34	205366_s_at	HOXB6	27.77	2.05E-37	2.17E-34	0.91	15.04	17q21.3
35	238756_at		3.96	3.63E-35	2.49E-32	0.90	14.95	
36	227853_at		2.99	1.28E-23	3.73E-21	1.03	14.92	
37	226134_s_at		4.97	1.99E-36	1.94E-33	0.88	14.79	
38	238455_at		4.30	4.84E-36	4.38E-33	0.88	14.75	
39	203680_at	PRKAR2B	5.66	1.36E-35	1.04E-32	0.87	14.62	7q22-q31.1
40	213908_at		5.31	3.40E-35	2.39E-32	0.87	14.59	
41	204030_s_at	SCHIP1	16.16	6.78E-36	5.73E-33	0.87	14.55	3q25.33
42	225240_s_at		4.31	7.68E-35	5.12E-32	0.85	14.40	
43	208146_s_at	CPVL	13.73	1.48E-35	1.10E-32	0.85	14.37	7p15-p14
44	203741_s_at	ADCY7	4.64	3.06E-30	1.41E-27	0.88	14.28	16q12-q13
45	220377_at	C14orf110	104.32	6.90E-34	4.35E-31	0.86	14.07	14q32.33
46	229971_at	GPR114	6.58	1.80E-30	8.76E-28	0.86	14.03	16q12.2
47	206478_at	KIAA0125	9.86	8.86E-34	5.34E-31	0.84	13.98	14q32.33
48	243010_at	MSI2	3.25	1.10E-33	6.46E-31	0.82	13.94	17q23.1
49	224764_at	ARHGAP10	5.87	1.87E-33	1.08E-30	0.82	13.88	
50	219062_s_at	FLJ20281	3.14	1.63E-26	6.26E-24	0.89	13.86	18q21.32
2.10	AML_t(15;17) versus AML_t(8;21)							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	209732_at	CLECSF2	-31.87	6.61E-16	1.83E-11	-3.41	-18.50	12p13-p12
2	214450_at	CTSW	32.70	1.75E-13	8.07E-10	3.62	17.85	11q13.1
3	38487_at	STAB1	23.73	4.75E-13	1.20E-09	3.30	16.70	3p21.31
4	211990_at	HLA-DPA1	-11.38	8.43E-15	1.17E-10	-2.54	-15.15	6p21.3
5	212509_s_at		10.56	1.02E-10	8.07E-08	2.39	12.28	

Note: Row 49 (224764_at ARHGAP10) shows "10" in the far right margin area.

6	221004_s_at	ITM2C	3.38	3.94E-13	1.20E-09	1.92	12.13	2q37
7	217478_s_at	HLA-DMA	-5.37	1.31E-13	8.07E-10	-1.90	-12.10	6p21.3
8	212953_x_at	CALR	2.46	4.33E-13	1.20E-09	1.86	11.84	19p13.3-p13.2
9	224839_s_at	GPT2	9.84	6.52E-11	6.28E-08	2.10	11.80	16q12.1
10	204150_at	STAB1	26.03	3.22E-10	1.88E-07	2.39	11.71	3p21.31
11	226878_at		-5.22	3.86E-12	7.65E-09	-1.95	-11.66	
12	205663_at	PCBP3	4.49	1.54E-11	2.38E-08	1.95	11.65	21q22.3
13	201596_x_at	KRT18	23.76	3.19E-10	1.88E-07	2.32	11.63	12q13
14	204316_at	RGS10	-2.58	2.53E-13	8.78E-10	-1.78	-11.47	10q25
15	205349_at	GNA15	3.44	3.85E-11	4.45E-08	1.90	11.27	19p13.3
16	211991_s_at	HLA-DPA1	-17.13	2.84E-11	3.58E-08	-1.96	-11.15	6p21.3
17	208689_s_at	RPN2	1.81	1.12E-13	8.07E-10	1.61	10.80	20q12-q13.1
18	209619_at	CD74	-4.53	1.48E-13	8.07E-10	-1.62	-10.79	5q32
19	200986_at	SERPING1	10.67	1.48E-09	6.06E-07	2.04	10.51	11q12-q13.1
20	208826_x_at	HINT1	1.43	2.32E-13	8.78E-10	1.56	10.48	5q31.2
21	227326_at		5.21	3.26E-10	1.88E-07	1.81	10.47	
22	204319_s_at	RGS10	-5.48	8.04E-11	7.19E-08	-1.76	-10.34	10q25
23	209312_x_at	HLA-DRB1	-6.71	1.16E-11	1.89E-08	-1.63	-10.33	6p21.3
24	201522_x_at	SNRPN	-3.69	5.83E-13	1.35E-09	-1.55	-10.31	15q12
25	211474_s_at	SERPINB6	-5.66	8.59E-11	7.28E-08	-1.73	-10.26	6p25
26	217716_s_at	SEC61A1	1.98	7.38E-12	1.36E-08	1.57	10.18	3q21.3
27	228113_at	STAT3	-4.67	2.42E-11	3.20E-08	-1.62	-10.17	17q21
28	200953_s_at	CCND2	2.76	4.76E-10	2.49E-07	1.73	10.12	12p13
29	228827_at		-103.40	4.47E-10	2.43E-07	-1.98	-10.04	
30	207721_x_at	HINT1	1.57	1.19E-12	2.54E-09	1.48	9.94	5q31.2
31	208306_x_at	HLA-DRB4	-6.81	4.41E-11	4.89E-08	-1.57	-9.88	6p21.3
32	227353_at	EVER2	-3.90	1.85E-11	2.70E-08	-1.53	-9.83	17q25.3
33	201137_s_at	HLA-DPB1	-12.31	4.76E-10	2.49E-07	-1.76	-9.82	6p21.3
34	208852_s_at	CANX	2.25	8.79E-11	7.28E-08	1.55	9.79	5q35
35	238022_at		4.12	1.01E-11	1.76E-08	1.47	9.70	
36	201923_at	PRDX4	-6.62	1.94E-10	1.38E-07	-1.60	-9.69	Xp22.13
37	218795_at	ACP6	-2.77	4.94E-11	5.27E-08	-1.50	-9.56	1q21
38	206940_s_at	POU4F1	-45.36	1.38E-09	5.89E-07	-1.87	-9.48	13q21.1-q22
39	205614_x_at	MST1	6.64	5.11E-09	1.59E-06	1.73	9.46	3p21
40	223321_s_at	FGFRL1	4.08	3.37E-09	1.17E-06	1.65	9.40	4p16
41	205771_s_at	AKAP7	-5.88	1.70E-10	1.28E-07	-1.50	-9.39	6q23
42	215193_x_at	HLA-DRB1	-6.64	5.32E-11	5.46E-08	-1.45	-9.35	6p21.3
43	222307_at	LOC282997	-2.74	3.08E-11	3.71E-08	-1.43	-9.34	10q25.2
44	55093_at	CSGlcA-T	1.90	3.36E-10	1.90E-07	1.49	9.33	7q36.1
45	201952_at	ALCAM	4.60	2.47E-09	9.13E-07	1.58	9.27	3q13.1
46	201136_at	PLP2	2.92	7.82E-11	7.19E-08	1.42	9.25	Xp11.23
47	221865_at	DKFZp547P234	-3.09	8.93E-11	7.28E-08	-1.43	-9.21	9q33.1
48	205529_s_at	CBFA2T1	-14.51	2.28E-09	8.69E-07	-1.73	-9.18	8q22
49	224356_x_at	MS4A6A	-6.39	9.01E-10	4.23E-07	-1.55	-9.18	11q12.1
50	202732_at	PKIG	2.71	2.63E-09	9.36E-07	1.55	9.17	20q12-q13.1

Table 3

3. One-Versus-All (OVA)							
3.1 denovo_AML versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	236892_s_at		6.31	4.24E-24	1.67E-19	0.57	10.92	
2	239791_at		5.75	3.02E-23	5.97E-19	0.56	10.72	
3	228904_at		4.04	1.10E-18	1.45E-14	0.53	9.75	
4	201069_at	MMP2	3.63	1.77E-15	1.74E-11	0.47	8.59	16q13-q21
5	228994_at	MGC45441	2.40	5.62E-15	4.44E-11	0.44	8.23	1p34.1
6	231175_at	FLJ30162	3.34	1.37E-13	9.03E-10	0.44	7.99	6p11.1
7	232979_at		2.40	5.69E-12	3.21E-08	0.45	7.69	
8	231767_at	HOXB4	1.87	3.32E-10	1.46E-06	0.44	7.10	17q21-q22
9	213217_at	ADCY2	4.27	4.55E-11	2.25E-07	0.35	6.79	5p15.3
10	204501_at	NOV	1.78	7.71E-10	3.05E-06	0.36	6.49	8q24.1
11	201029_s_at	CD99	1.48	8.84E-08	2.05E-04	0.50	6.36	Xp22.32
12	214321_at	NOV	2.97	9.13E-10	3.28E-06	0.34	6.35	8q24.1
13	238021_s_at		2.66	4.01E-08	1.05E-04	0.43	6.26	
14	239151_at		1.48	2.42E-08	7.07E-05	0.37	6.11	
15	235092_at		1.66	6.38E-08	1.57E-04	0.39	6.02	
16	244607_at		1.77	2.51E-08	7.07E-05	0.35	5.97	
17	201028_s_at	CD99	1.91	2.09E-07	4.34E-04	0.42	5.93	Xp22.32
18	201481_s_at	PYGB	2.17	1.39E-08	4.59E-05	0.30	5.81	20p11.2-p11.1
19	238022_at		2.68	3.50E-07	6.59E-04	0.40	5.77	
20	243134_at		1.47	6.73E-07	1.11E-03	0.39	5.59	
21	236738_at		2.68	2.59E-07	5.12E-04	0.32	5.48	
22	230743_at		1.52	6.32E-07	1.08E-03	0.35	5.43	
23	226461_at	HOXB9	1.57	2.05E-07	4.34E-04	0.29	5.35	17q21.3
24	235265_at		1.80	1.44E-06	1.75E-03	0.35	5.29	
25	205453_at	HOXB2	2.19	3.00E-06	3.12E-03	0.39	5.27	17q21-q22
26	214110_s_at		1.79	3.88E-07	6.96E-04	0.29	5.25	
27	235273_at	EKN1	2.12	2.77E-06	2.96E-03	0.37	5.22	15q21.1
28	205601_s_at	HOXB5	1.67	2.36E-06	2.59E-03	0.35	5.21	17q21.3
29	214455_at	HIST1H2BC	2.01	7.85E-07	1.19E-03	0.30	5.19	6p21.3
30	229309_at		2.36	9.05E-07	1.28E-03	0.30	5.18	
31	202708_s_at	HIST2H2BE	1.81	2.34E-06	2.59E-03	0.34	5.17	1q21-q23
32	205899_at	CCNA1	2.10	1.14E-06	1.55E-03	0.31	5.16	13q12.3-q13
33	227752_at		2.30	1.21E-06	1.59E-03	0.31	5.15	
34	236893_at		2.44	1.57E-06	1.82E-03	0.32	5.15	
35	205366_s_at	HOXB6	3.24	3.83E-06	3.77E-03	0.36	5.12	17q21.3
36	209702_at	MGC5149	1.71	7.71E-07	1.19E-03	0.28	5.11	16q12.1
37	202088_at	LIV-1	1.34	4.01E-06	3.77E-03	0.36	5.11	18q12.1
38	242904_x_at	MGC8721	1.72	3.92E-06	3.77E-03	0.35	5.07	8p12

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
39	201522_x_at	SNRPN	-1.44	8.49E-06	6.98E-03	-0.41	-5.05	15q12
40	244889_at		2.07	8.90E-07	1.28E-03	0.27	5.04	
41	237108_x_at	DKFZp761G0122	1.87	1.46E-06	1.75E-03	0.28	5.00	1p36.32
42	215948_x_at	ZNF237	1.41	6.31E-06	5.66E-03	0.36	5.00	13q12
43	206134_at	ADAMDEC1	1.93	1.25E-06	1.60E-03	0.26	4.94	8p21.1
44	205624_at	CPA3	2.63	1.10E-05	8.08E-03	0.35	4.87	3q21-q25
45	244048_x_at		2.33	3.87E-06	3.77E-03	0.29	4.86	
46	235637_s_at		1.87	9.58E-06	7.63E-03	0.32	4.82	
47	243348_at		1.86	1.09E-05	8.08E-03	0.32	4.76	
48	209098_s_at	JAG1	1.76	7.85E-06	6.59E-03	0.28	4.70	20p12.1-p11.23
49	236470_at		2.02	6.74E-06	5.91E-03	0.27	4.69	
50	213479_at	NPTX2	3.18	5.06E-06	4.64E-03	0.26	4.68	7q21.3-q22.1

3.2 s_AML versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214757_at	PMS2L9	-3.32	3.62E-20	1.47E-15	-0.56	-10.36	7q11.23
2	236893_at		-4.03	3.17E-19	6.45E-15	-0.51	-9.66	
3	205179_s_at	ADAM8	-3.35	3.98E-13	2.25E-09	-0.57	-9.49	10q26.3
4	229319_at		-3.12	2.56E-17	3.47E-13	-0.51	-9.43	
5	210783_x_at	SCGF	-3.70	6.29E-12	2.13E-08	-0.58	-9.34	19q13.3
6	212009_s_at	STIP1	-6.28	1.07E-14	7.40E-11	-0.51	-9.04	11q13
7	228678_at		-3.58	7.11E-12	2.23E-08	-0.56	-9.03	
8	241238_at		-3.23	1.51E-12	5.60E-09	-0.54	-9.02	
9	204561_x_at	APOC2	-14.22	1.24E-15	1.26E-11	-0.44	-8.37	19q13.2
10	222222_s_at		-5.37	1.09E-14	7.40E-11	-0.45	-8.37	
11	208579_x_at	HIST1H2BK	-2.31	1.29E-09	2.62E-06	-0.55	-8.34	6p21.33
12	219254_at	FLJ22222	-3.11	1.44E-07	1.03E-04	-0.64	-8.15	17q25.3
13	209958_s_at	B1	-2.47	4.42E-13	2.25E-09	-0.45	-8.10	7p14
14	230872_s_at	DKFZP434B103	-3.24	4.37E-07	2.41E-04	-0.68	-8.00	3p25.3
15	205131_x_at	SCGF	-3.48	9.92E-09	1.15E-05	-0.55	-8.00	19q13.3
16	239791_at		-3.87	3.04E-10	6.88E-07	-0.48	-7.87	
17	205081_at	CRIP1	-2.86	6.29E-08	5.33E-05	-0.55	-7.67	7q11.23
18	201028_s_at	CD99	-2.29	2.29E-07	1.42E-04	-0.59	-7.67	Xp22.32
19	236892_s_at		-4.85	4.30E-09	6.26E-06	-0.49	-7.66	
20	208534_s_at	CAPRI	-3.17	2.71E-08	2.63E-05	-0.52	-7.62	7q22-q31.1
21	243358_at	MGC18216	-1.68	7.93E-13	3.59E-09	-0.41	-7.61	15q26.3
22	218280_x_at	HIST2H2AA	-2.25	8.03E-07	4.02E-04	-0.64	-7.60	1q21.2
23	206735_at	CHRNA4	-2.19	2.03E-07	1.31E-04	-0.57	-7.54	20q13.2-q13.3
24	215501_s_at	DUSP10	-2.02	8.09E-07	4.02E-04	-0.62	-7.48	1q41
25	221759_at	LOC92579	-3.00	8.49E-08	6.78E-05	-0.52	-7.41	17q21.31
26	235700_at	MGC27005	-14.67	9.27E-13	3.77E-09	-0.39	-7.40	Xq26.3
27	230460_at		-2.48	5.39E-08	4.83E-05	-0.51	-7.37	

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
28	226781_at		-3.92	5.97E-10	1.28E-06	-0.43	-7.27	
29	236738_at		-2.91	1.79E-11	4.90E-08	-0.40	-7.26	
30	224699_s_at	KIAA1228	-1.77	3.28E-06	1.20E-03	-0.66	-7.21	7q36.3
31	231804_at	LGR7	-4.74	1.81E-11	4.90E-08	-0.38	-7.12	4q32.1
32	227824_at		-2.32	1.65E-09	3.20E-06	-0.43	-7.12	
33	240235_at		-1.92	1.69E-07	1.15E-04	-0.49	-7.06	
34	231175_at	FLJ30162	-4.04	8.88E-08	6.95E-05	-0.48	-7.03	6p11.1
35	226694_at	AKAP2	-2.87	1.27E-06	5.66E-04	-0.55	-6.99	9q31-q33
36	201203_s_at	RRBP1	-2.05	6.64E-09	8.50E-06	-0.42	-6.92	20p12
37	237974_at		-3.65	5.21E-11	1.33E-07	-0.37	-6.91	
38	214290_s_at	HIST2H2AA	-2.20	9.79E-06	3.00E-03	-0.69	-6.90	1q21.2
39	223360_at	DKFZp434N0650	-2.06	9.87E-08	7.58E-05	-0.46	-6.86	21q22.3
40	222974_at	IL22	-2.62	3.50E-08	3.32E-05	-0.44	-6.85	12q15
41	235063_at	FLJ25067	-2.06	1.07E-07	7.96E-05	-0.46	-6.84	20p12.3
42	205479_s_at	PLAU	-2.01	3.05E-07	1.83E-04	-0.47	-6.80	10q24
43	229461_x_at	MGC46680	-3.64	2.87E-09	4.67E-06	-0.40	-6.80	1p31.1
44	217613_at		-2.24	2.67E-09	4.67E-06	-0.40	-6.78	
45	214724_at	KIAA1735	-2.62	9.07E-07	4.29E-04	-0.50	-6.74	
46	200897_s_at	KIAA0992	-3.82	1.63E-08	1.84E-05	-0.41	-6.72	4q32.3
47	220311_at	N6AMT1	-2.82	6.50E-09	8.50E-06	-0.40	-6.72	21q21.3
48	206622_at	TRH	-8.56	9.69E-11	2.32E-07	-0.35	-6.67	3q13.3-q21
49	236423_at		-2.79	2.82E-09	4.67E-06	-0.38	-6.66	
50	218788_s_at	FLJ21080	-2.16	2.43E-06	9.41E-04	-0.52	-6.64	1q44

3.3 t_AML versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	236892_s_at		-7.02	1.15E-25	4.47E-21	-0.59	-11.35	
2	239791_at		-7.13	8.48E-23	1.65E-18	-0.59	-10.89	
3	201069_at	MMP2	-4.94	3.34E-21	4.33E-17	-0.55	-10.33	16q13-q21
4	235637_s_at		-2.47	7.58E-20	7.36E-16	-0.54	-10.00	
5	228904_at		-5.04	1.12E-15	8.72E-12	-0.56	-9.59	
6	205366_s_at	HOXB6	-6.74	9.55E-14	6.19E-10	-0.54	-8.93	17q21.3
7	232979_at		-2.59	6.16E-12	2.66E-08	-0.50	-8.15	
8	228994_at	MGC45441	-2.35	2.58E-13	1.43E-09	-0.43	-7.86	1p34.1
9	243829_at	BRAF	-1.61	1.20E-09	2.75E-06	-0.54	-7.75	7q34
10	216973_s_at	HOXB7	-2.30	1.79E-12	8.68E-09	-0.43	-7.65	17q21.3
11	238022_at		-2.87	2.83E-10	9.15E-07	-0.49	-7.59	
12	237891_at	MDM2	-2.30	1.77E-10	6.25E-07	-0.42	-7.11	12q14.3-q15
13	213217_at	ADCY2	-4.82	7.56E-12	2.94E-08	-0.37	-7.08	5p15.3
14	242904_x_at	MGC8721	-2.09	6.94E-09	1.28E-05	-0.48	-7.05	8p12
15	214360_at	SMARCA4	-1.98	1.46E-09	3.16E-06	-0.42	-6.88	19p13.13
16	204779_s_at	HOXB7	-2.33	3.28E-10	9.81E-07	-0.39	-6.87	17q21.3
17	227752_at		-2.95	5.37E-10	1.49E-06	-0.40	-6.83	
18	231175_at	FLJ30162	-2.95	4.44E-09	9.08E-06	-0.41	-6.63	6p11.1

19	204501_at	NOV	-1.80	9.65E-10	2.50E-06	-0.38	-6.62	8q24.1
20	230743_at		-1.64	1.48E-08	2.50E-05	-0.43	-6.61	
21	233840_at		-1.99	1.35E-08	2.39E-05	-0.42	-6.56	
22	214321_at	NOV	-3.39	1.13E-09	2.73E-06	-0.36	-6.50	8q24.1
23	231767_at	HOXB4	-2.07	1.40E-07	1.86E-04	-0.48	-6.48	17q21-q22
24	240128_at		-2.13	1.73E-07	1.98E-04	-0.48	-6.46	
25	240008_at		-1.73	1.27E-07	1.83E-04	-0.47	-6.45	
26	238389_s_at		-1.58	2.96E-07	3.02E-04	-0.49	-6.37	
27	215948_x_at	ZNF237	-1.63	3.86E-07	3.75E-04	-0.50	-6.33	13q12
28	205601_s_at	HOXB5	-1.91	1.62E-07	1.90E-04	-0.45	-6.33	17q21.3
29	233224_at		-1.50	3.45E-08	5.58E-05	-0.40	-6.32	
30	244360_at		-1.59	1.53E-07	1.90E-04	-0.44	-6.28	
31	238303_at		-2.03	1.59E-07	1.90E-04	-0.44	-6.26	
32	238021_s_at		-2.72	4.65E-07	4.20E-04	-0.45	-6.08	
33	244607_at		-1.86	7.54E-08	1.13E-04	-0.38	-6.07	
34	213437_at	RIPX	-2.47	2.44E-07	2.63E-04	-0.42	-6.07	4q13.3
35	215102_at	LOC89231	-2.32	1.42E-07	1.86E-04	-0.40	-6.07	7p14.3
36	244889_at		-2.31	5.40E-09	1.05E-05	-0.32	-6.02	
37	235587_at	LOC202781	-1.67	1.47E-06	1.04E-03	-0.48	-5.95	7q36.3
38	205453_at	HOXB2	-3.02	2.36E-06	1.50E-03	-0.50	-5.87	17q21-q22
39	204485_s_at	TOM1L1	-2.04	4.48E-07	4.14E-04	-0.39	-5.81	17q23.2
40	239829_at		-1.87	1.77E-06	1.21E-03	-0.43	-5.71	
41	207063_at	CYorf14	-2.36	1.98E-07	2.20E-04	-0.35	-5.71	Yq11.221
42	220211_at	FLJ13224	-1.80	3.38E-07	3.37E-04	-0.36	-5.70	12p11.21
43	229620_at	SEPP1	-3.05	6.29E-07	5.43E-04	-0.38	-5.70	5q31
44	226150_at	HTPAP	-1.61	4.35E-06	2.32E-03	-0.49	-5.68	8p11.21
45	207111_at	EMR1	-1.90	7.48E-07	6.05E-04	-0.37	-5.63	19p13.3
46	204944_at	PTPRG	-3.20	3.88E-08	6.03E-05	-0.30	-5.63	3p21-p14
47	203313_s_at	TGIF	-1.83	5.33E-06	2.72E-03	-0.47	-5.58	18p11.3
48	231165_at		-1.91	2.95E-06	1.79E-03	-0.41	-5.53	
49	213110_s_at	COL4A5	-3.42	3.62E-06	2.07E-03	-0.41	-5.47	Xq22
50	235288_at		-1.62	1.38E-06	9.90E-04	-0.36	-5.44	

Table 4

4. All-Pairs (AP)

4.1 denovo_AML versus s_AML

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214757_at	PMS2L9	3.22	1.02E-18	2.05E-14	0.55	9.87	7q11.23
2	236893_at		4.16	4.59E-19	1.84E-14	0.52	9.60	
3	205179_s_at	ADAM8	3.27	1.40E-12	6.23E-09	0.58	9.26	10q26.3
4	210783_x_at	SCGF	3.64	1.29E-11	3.69E-08	0.59	9.13	19q13.3
5	229319_at		3.05	2.38E-16	3.18E-12	0.51	9.08	
6	228678_at		3.63	3.86E-12	1.40E-08	0.56	9.02	
7	241238_at		3.26	9.95E-13	4.98E-09	0.55	8.93	
8	212009_s_at	STIP1	6.12	4.94E-14	3.30E-10	0.51	8.73	11q13
9	222222_s_at		5.47	1.66E-14	1.66E-10	0.46	8.27	
10	239791_at		4.08	4.53E-11	1.21E-07	0.51	8.21	
11	208579_x_at	HIST1H2BK	2.31	1.26E-09	2.52E-06	0.54	8.15	6p21.33
12	209958_s_at	B1	2.53	2.44E-13	1.40E-09	0.46	8.13	7p14
13	219254_at	FLJ22222	3.08	1.57E-07	1.10E-04	0.64	7.99	17q25.3
14	230872_s_at	DKFZP434B103	3.25	3.48E-07	2.11E-04	0.68	7.98	3p25.3
15	236892_s_at		5.11	8.80E-10	1.86E-06	0.52	7.98	
16	201028_s_at	CD99	2.35	1.01E-07	7.77E-05	0.61	7.92	Xp22.32
17	204561_x_at	APOC2	13.86	3.69E-14	2.95E-10	0.43	7.91	19q13.2
18	205131_x_at	SCGF	3.44	1.41E-08	1.82E-05	0.55	7.82	19q13.3
19	218280_x_at	HIST2H2AA	2.29	4.79E-07	2.78E-04	0.65	7.76	1q21.2
20	208534_s_at	CAPRI	3.21	1.87E-08	2.14E-05	0.54	7.68	7q22-q31.1
21	215501_s_at	DUSP10	2.05	5.00E-07	2.82E-04	0.64	7.68	1q41
22	205081_at	CRIP1	2.85	6.95E-08	6.05E-05	0.55	7.55	7q11.23
23	243358_at	MGC18216	1.69	1.74E-12	6.99E-09	0.41	7.47	15q26.3
24	206735_at	CHRNA4	2.18	2.09E-07	1.34E-04	0.56	7.39	20q13.2-q13.3
25	236738_at		3.01	7.76E-12	2.59E-08	0.41	7.36	
26	221759_at	LOC92579	3.01	7.10E-08	6.05E-05	0.52	7.33	17q21.31
27	231175_at	FLJ30162	4.20	2.99E-08	3.05E-05	0.49	7.25	6p11.1
28	230460_at		2.48	5.49E-08	5.00E-05	0.50	7.23	
29	226781_at		3.70	2.91E-09	5.30E-06	0.45	7.20	
30	224699_s_at	KIAA1228	1.77	3.36E-06	1.26E-03	0.66	7.15	7q36.3
31	235700_at	MGC27005	13.80	1.01E-11	3.12E-08	0.38	7.05	Xq26.3
32	227824_at		2.31	2.24E-09	4.27E-06	0.43	7.01	
33	214290_s_at	HIST2H2AA	2.22	7.64E-06	2.55E-03	0.71	7.00	1q21.2
34	226694_at	AKAP2	2.88	1.09E-06	5.30E-04	0.55	6.95	9q31-q33
35	231804_at	LGR7	4.67	8.28E-11	2.07E-07	0.38	6.85	4q32.1
36	223360_at	DKFZp434N0650	2.07	7.50E-08	6.17E-05	0.46	6.83	21q22.3
37	228904_at		2.87	1.19E-07	8.96E-05	0.47	6.83	
38	201203_s_at	RRBP1	2.05	7.98E-09	1.18E-05	0.42	6.81	20p12
39	205479_s_at	PLAU	2.02	2.11E-07	1.34E-04	0.48	6.81	10q24
40	237974_at		3.72	1.06E-10	2.50E-07	0.37	6.77	

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
41	229461_x_at	MGC46680	3.63	3.60E-09	6.26E-06	0.40	6.73	1p31.1
42	214724_at	KIAA1735	2.62	8.14E-07	4.08E-04	0.50	6.68	
43	240235_at		1.87	3.88E-07	2.32E-04	0.48	6.67	
44	218788_s_at	FLJ21080	2.18	1.85E-06	7.78E-04	0.52	6.65	1q44
45	222974_at	IL22	2.60	5.20E-08	4.84E-05	0.43	6.64	12q15
46	202708_s_at	HIST2H2BE	2.18	7.93E-07	4.02E-04	0.48	6.58	1q21-q23
47	222693_at	FAD104	2.19	5.99E-07	3.20E-04	0.47	6.57	3q26.31
48	206622_at	TRH	8.74	2.04E-10	4.53E-07	0.35	6.56	3q13.3-q21
49	217613_at		2.22	6.53E-09	1.01E-05	0.39	6.51	
50	220311_at	N6AMT1	2.71	2.19E-08	2.37E-05	0.40	6.51	21q21.3

4.2 denovo_AML versus t_AML

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	236892_s_at		7.20	7.11E-26	2.74E-21	0.61	11.43	
2	239791_at		7.31	3.94E-23	7.58E-19	0.60	10.97	
3	201069_at	MMP2	5.03	2.80E-21	3.59E-17	0.56	10.34	16q13-q21
4	235637_s_at		2.49	1.11E-19	1.07E-15	0.54	9.93	
5	228904_at		5.14	4.32E-16	3.32E-12	0.57	9.69	
6	205366_s_at	HOXB6	6.83	6.33E-14	4.06E-10	0.54	8.95	17q21.3
7	232979_at		2.64	2.82E-12	1.21E-08	0.51	8.26	
8	228994_at	MGC45441	2.40	1.27E-13	6.99E-10	0.44	7.95	1p34.1
9	238022_at		2.92	1.31E-10	4.58E-07	0.50	7.74	
10	243829_at	BRAF	1.60	1.56E-09	3.53E-06	0.54	7.62	7q34
11	216973_s_at	HOXB7	2.30	2.18E-12	1.05E-08	0.43	7.61	17q21.3
12	242904_x_at	MGC8721	2.10	5.25E-09	1.01E-05	0.48	7.08	8p12
13	213217_at	ADCY2	4.93	7.77E-12	2.99E-08	0.38	7.08	5p15.3
14	237891_at	MDM2	2.31	1.91E-10	6.12E-07	0.42	7.06	12q14.3-q15
15	227752_at		2.99	4.37E-10	1.20E-06	0.40	6.84	
16	204779_s_at	HOXB7	2.34	3.92E-10	1.16E-06	0.39	6.81	17q21.3
17	231175_at	FLJ30162	3.02	1.89E-09	4.04E-06	0.42	6.79	6p11.1
18	214360_at	SMARCA4	1.96	3.03E-09	6.14E-06	0.41	6.70	19p13.13
19	204501_at	NOV	1.83	5.70E-10	1.46E-06	0.38	6.70	8q24.1
20	230743_at		1.65	1.01E-08	1.77E-05	0.43	6.67	
21	231767_at	HOXB4	2.09	9.13E-08	1.30E-04	0.48	6.57	17q21-q22
22	214321_at	NOV	3.45	8.30E-10	1.99E-06	0.37	6.54	8q24.1
23	233840_at		1.98	2.11E-08	3.52E-05	0.42	6.46	
24	238389_s_at		1.58	2.41E-07	2.51E-04	0.49	6.41	
25	205601_s_at	HOXB5	1.93	1.20E-07	1.65E-04	0.46	6.39	17q21.3
26	240128_at		2.12	2.27E-07	2.49E-04	0.48	6.35	
27	215948_x_at	ZNF237	1.63	3.32E-07	3.12E-04	0.50	6.35	13q12
28	240008_at		1.72	2.00E-07	2.42E-04	0.46	6.29	
29	244360_at		1.59	1.46E-07	1.94E-04	0.44	6.27	
30	238021_s_at		2.78	2.67E-07	2.70E-04	0.46	6.23	
31	233224_at		1.50	4.62E-08	7.34E-05	0.40	6.21	
32	244607_at		1.88	4.83E-08	7.34E-05	0.39	6.15	
33	213437_at	RIPX	2.48	2.35E-07	2.51E-04	0.42	6.07	4q13.3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
34	238303_at		2.00	2.96E-07	2.92E-04	0.43	6.06	
35	244889_at		2.34	5.67E-09	1.04E-05	0.32	6.01	
36	215102_at	LOC89231	2.31	1.78E-07	2.28E-04	0.39	5.97	7p14.3
37	205453_at	HOXB2	3.05	1.89E-06	1.27E-03	0.50	5.93	17q21-q22
38	235587_at	LOC202781	1.66	1.72E-06	1.25E-03	0.48	5.87	7q36.3
39	204485_s_at	TOM1L1	2.03	5.40E-07	4.70E-04	0.39	5.74	17q23.2
40	229620_at	SEPP1	3.07	5.50E-07	4.70E-04	0.38	5.70	5q31
41	220211_at	FLJ13224	1.81	3.27E-07	3.12E-04	0.36	5.69	12p11.21
42	207063_at	CYorf14	2.36	2.24E-07	2.49E-04	0.35	5.66	Yq11.221
43	226150_at	HTPAP	1.61	4.71E-06	2.67E-03	0.49	5.63	8p11.21
44	207111_at	EMR1	1.91	6.60E-07	5.30E-04	0.37	5.63	19p13.3
45	239829_at		1.85	2.80E-06	1.74E-03	0.44	5.61	
46	204944_at	PTPRG	3.24	4.96E-08	7.34E-05	0.30	5.58	3p21-p14
47	203313_s_at	TGIF	1.83	5.42E-06	2.90E-03	0.47	5.55	18p11.3
48	213110_s_at	COL4A5	3.47	2.66E-06	1.70E-03	0.42	5.55	Xq22
49	231165_at		1.91	2.72E-06	1.72E-03	0.41	5.53	
50	226461_at	HOXB9	1.62	2.01E-07	2.42E-04	0.31	5.45	17q21.3

4.3 s_AML versus t_AML

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	214000_s_at	RGS10	1.89	3.15E-05	8.24E-01	0.92	5.08	10q25
2	204316_at	RGS10	1.66	1.25E-04	8.24E-01	0.93	4.87	10q25
3	242557_at		2.33	1.89E-04	8.24E-01	0.90	4.71	
4	236189_at		2.75	1.52E-04	8.24E-01	0.82	4.52	
5	241101_at		2.43	1.84E-04	8.24E-01	0.81	4.45	
6	240222_at		2.21	4.11E-04	8.24E-01	0.85	4.39	
7	211205_x_at	PIP5K1A	-3.63	1.66E-04	8.24E-01	-0.79	-4.37	1q22-q24
8	240235_at		-2.62	2.38E-04	8.24E-01	-0.82	-4.34	
9	229143_at	CNOT3	1.66	5.01E-04	8.24E-01	0.84	4.30	19q13.4
10	240046_at		1.94	2.11E-04	8.24E-01	0.77	4.30	
11	242853_at		1.68	4.77E-04	8.24E-01	0.82	4.29	
12	205329_s_at	SNX4	-1.71	1.98E-04	8.24E-01	-0.75	-4.24	3q21.2
13	228412_at	BAZ2B	-2.26	2.03E-04	8.24E-01	-0.75	-4.23	2q23-q24
14	213763_at		1.93	3.17E-04	8.24E-01	0.76	4.18	
15	242760_x_at		-2.37	3.30E-04	8.24E-01	-0.76	-4.16	
16	205008_s_at	KIP2	-2.15	2.95E-04	8.24E-01	-0.73	-4.12	15q24
17	214995_s_at	APOBEC3G	-2.17	2.96E-04	8.24E-01	-0.73	-4.11	22q13.1-q13.2
18	220916_at	FLJ13310	1.77	2.92E-04	8.24E-01	0.73	4.10	1q32.1
19	216888_at	LDB3	-1.52	3.64E-04	8.24E-01	-0.71	-4.02	10q22.3-q23.2
20	236208_at		2.24	1.60E-03	8.24E-01	0.86	4.01	
21	230872_s_at	DKFZP434B103	-2.98	4.87E-04	8.24E-01	-0.70	-3.93	3p25.3
22	219254_at	FLJ22222	-3.51	6.06E-04	8.24E-01	-0.72	-3.92	17q25.3
23	209896_s_at	MGC14433	-1.59	4.87E-04	8.24E-01	-0.69	-3.92	12q24.13
24	217225_x_at	LOC283820	-1.58	5.18E-04	8.24E-01	-0.70	-3.91	16p13.13
25	212811_x_at	PSA	-2.02	5.48E-04	8.24E-01	-0.69	-3.89	9q21.2
26	230054_at		2.40	2.58E-03	8.24E-01	0.93	3.89	

27 242299_at		1.85	1.60E-03	8.24E-01	0.79	3.88	
28 227874_at		2.24	1.25E-03	8.24E-01	0.72	3.80	
29 233643_at		1.56	7.42E-04	8.24E-01	0.67	3.79	
30 206735_at	CHRNA4	-2.35	8.55E-04	8.24E-01	-0.69	-3.78	20q13.2-q13.3
31 235753_at		-2.73	8.68E-04	8.24E-01	-0.69	-3.77	
32 235587_at	LOC202781	1.84	1.87E-03	8.24E-01	0.75	3.76	7q36.3
33 238860_at	MGC19570	1.65	1.23E-03	8.24E-01	0.70	3.74	6p21.1
34 204082_at	PBX3	-4.16	1.14E-03	8.24E-01	-0.71	-3.73	9q33-q34
35 222425_s_at	DKFZP586F1524	-2.48	8.56E-04	8.24E-01	-0.66	-3.71	17q11.1
36 214388_at		-1.75	8.64E-04	8.24E-01	-0.66	-3.71	
37 209389_x_at	DBI	-1.79	8.56E-04	8.24E-01	-0.66	-3.71	2q12-q21
38 207531_at	CRYGC	-2.00	8.62E-04	8.24E-01	-0.66	-3.70	2q33-q35
39 240090_at		2.13	2.66E-03	8.24E-01	0.78	3.69	
40 223354_x_at	GL004	1.36	1.12E-03	8.24E-01	0.66	3.68	2q36.3
41 236604_at	FLJ23058	-1.55	1.00E-03	8.24E-01	-0.65	-3.67	17q25.3
42 238729_x_at	SAV1	1.78	1.34E-03	8.24E-01	0.67	3.66	14q13-q23
43 239655_at		1.68	2.04E-03	8.24E-01	0.71	3.65	
44 203725_at	GADD45A	1.90	1.33E-03	8.24E-01	0.66	3.63	1p31.2-p31.1
45 208579_x_at	HIST1H2BK	-2.39	1.35E-03	8.24E-01	-0.68	-3.63	6p21.33
46 221475_s_at	RPL15	1.21	2.22E-03	8.24E-01	0.71	3.63	3p24.1
47 214757_at	PMS2L9	-4.98	1.68E-03	8.24E-01	-0.75	-3.62	7q11.23
48 244451_x_at		1.79	1.64E-03	8.24E-01	0.67	3.61	
49 239140_at		1.73	1.92E-03	8.24E-01	0.68	3.61	
50 219219_at	FLJ20512	-1.67	1.10E-03	8.24E-01	-0.64	-3.61	19q13.32

Table 5

5. One-Versus-All (OVA)							
5.1	AML M0 versus rest						
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213110_s_at	COL4A5	-8.84	4.55E-26	1.50E-21	-0.82	-12.19	Xq22
2	209099_x_at	JAG1	-6.57	1.46E-24	2.40E-20	-0.84	-12.15	20p12.1-p11.23
3	205366_s_at	HOXB6	-9.06	5.21E-23	5.71E-19	-0.81	-11.75	17q21.3
4	216268_s_at	JAG1	-6.18	1.29E-22	1.06E-18	-0.79	-11.45	20p12.1-p11.23
5	236892_s_at		-7.42	4.41E-21	2.90E-17	-0.77	-11.05	
6	235749_at	UGCGL2	-5.24	3.96E-18	1.30E-14	-0.79	-10.94	13q32.1
7	205653_at	CTSG	-6.04	5.11E-18	1.53E-14	-0.78	-10.83	14q11.2
8	242426_at	LOC145957	-4.22	1.04E-20	5.70E-17	-0.73	-10.64	15q23
9	212820_at	RC3	-3.88	3.15E-16	6.47E-13	-0.78	-10.55	15q15.3
10	227716_at	SOC	-4.95	1.97E-20	9.24E-17	-0.70	-10.35	1p35.3
11	219304_s_at	SCDGF-B	-3.00	2.28E-15	3.74E-12	-0.77	-10.29	11q22.3
12	202924_s_at	PLAGL2	-1.70	5.56E-15	8.30E-12	-0.76	-10.08	20q11.1
13	228904_at		-4.63	5.68E-16	1.10E-12	-0.72	-9.94	
14	218865_at	FLJ22390	-11.01	3.32E-19	1.36E-15	-0.68	-9.91	1q42.11
15	204779_s_at	HOXB7	-3.79	2.95E-18	1.08E-14	-0.65	-9.58	17q21.3
16	239791_at		-5.01	1.15E-15	2.11E-12	-0.69	-9.56	
17	218332_at	BEX1	-6.69	2.31E-16	5.42E-13	-0.66	-9.46	Xq21-q23
18	216973_s_at	HOXB7	-3.43	4.40E-17	1.21E-13	-0.64	-9.36	17q21.3
19	213823_at	HOXA11	-3.35	2.81E-15	4.40E-12	-0.66	-9.28	7p15-p14
20	226817_at		-4.05	2.59E-16	5.67E-13	-0.63	-9.19	
21	227889_at		-3.12	1.83E-11	1.22E-08	-0.75	-9.18	
22	223703_at	CDA017	-2.68	3.18E-10	1.47E-07	-0.80	-9.12	10q23.1
23	208967_s_at	AK2	-2.29	6.77E-12	4.94E-09	-0.72	-9.11	1p34
24	214575_s_at	AZU1	-6.11	2.39E-12	2.13E-09	-0.71	-9.09	19p13.3
25	212009_s_at	STIP1	-8.88	1.19E-16	3.01E-13	-0.61	-9.01	11q13
26	235413_at	GGCX	-2.54	8.23E-10	3.38E-07	-0.79	-8.90	2p12
27	202444_s_at	KEO4	-2.00	1.68E-12	1.68E-09	-0.66	-8.74	10q21-q22
28	204750_s_at	DSC2	-4.77	1.78E-15	3.08E-12	-0.60	-8.72	18q12.1
29	231183_s_at	JAG1	-2.67	1.85E-11	1.22E-08	-0.67	-8.62	20p12.1-p11.23
30	201069_at	MMP2	-4.77	6.55E-14	8.28E-11	-0.61	-8.60	16q13-q21
31	228497_at	FLIPT1	-3.02	1.85E-12	1.78E-09	-0.64	-8.58	1p13.1
32	236738_at		-7.54	2.81E-14	3.85E-11	-0.60	-8.56	
33	204647_at	HOMER3	-3.73	5.93E-12	4.43E-09	-0.65	-8.53	19p13.11
34	209098_s_at	JAG1	-4.31	8.26E-15	1.18E-11	-0.58	-8.52	20p12.1-p11.23
35	225599_s_at		-2.64	4.01E-11	2.44E-08	-0.67	-8.49	
36	205633_s_at	ALAS1	-2.23	2.74E-13	3.22E-10	-0.60	-8.42	3p21.1

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
37	205382_s_at	DF	-4.36	3.45E-09	1.25E-06	-0.75	-8.39	19p13.3
38	206643_at	HAL	-3.68	9.14E-12	6.53E-09	-0.63	-8.32	12q22-q24.1
39	214033_at	ABCC6	-2.39	3.78E-09	1.35E-06	-0.74	-8.27	16p13.1
40	205600_x_at	HOXB5	-1.88	2.75E-09	1.02E-06	-0.72	-8.21	17q21.3
41	201444_s_at	ATP6IP2	-1.51	3.15E-11	1.96E-08	-0.63	-8.21	Xq21
42	209906_at	C3AR1	-4.21	5.36E-13	5.51E-10	-0.58	-8.21	12p13.31
43	238058_at		-2.02	2.07E-10	1.03E-07	-0.66	-8.20	
44	216667_at		-4.58	2.93E-13	3.33E-10	-0.57	-8.17	
45	220110_s_at	NXF3	-7.59	2.95E-14	3.88E-11	-0.55	-8.15	Xq22-q23
46	205601_s_at	HOXB5	-2.35	1.03E-09	4.16E-07	-0.68	-8.11	17q21.3
47	206851_at	RNASE3	-4.22	2.60E-10	1.24E-07	-0.64	-8.09	14q24-q31
48	242963_at	MGC26963	-3.23	4.19E-09	1.46E-06	-0.69	-7.99	4q25
49	237108_x_at	DKFZp761G0122	-3.07	8.03E-14	9.77E-11	-0.54	-7.99	1p36.32
50	203676_at	GNS	-2.96	8.29E-11	4.39E-08	-0.61	-7.95	12q14

5.2 AML M1 versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213836_s_at	FLJ10055	-2.15	1.65E-13	2.18E-09	-0.53	-7.87	17q24.3
2	205033_s_at	DEFA1	-2.18	4.66E-13	2.18E-09	-0.55	-7.87	8p23.2-p23.1
3	222753_s_at	FLJ22649	-1.45	3.13E-13	2.18E-09	-0.53	-7.80	4q34.2
4	218728_s_at	HSPC163	-1.87	4.69E-13	2.18E-09	-0.53	-7.75	1q42.12
5	206861_s_at	CGGBP1	-1.30	8.20E-13	3.06E-09	-0.53	-7.72	3p12-p11.1
6	214084_x_at	NCF1	-3.70	1.22E-12	3.24E-09	-0.52	-7.59	7q11.23
7	204961_s_at	NCF1	-4.59	1.20E-12	3.24E-09	-0.51	-7.57	7q11.23
8	226240_at	MGC21874	-1.75	2.14E-12	4.97E-09	-0.51	-7.48	4p16.1
9	202917_s_at	S100A8	-1.71	2.42E-11	4.10E-08	-0.53	-7.29	1q21
10	206676_at	CEACAM8	-3.89	9.22E-12	1.91E-08	-0.49	-7.22	19q13.2
11	223584_s_at	DKFZP566C134	-1.69	3.45E-11	4.59E-08	-0.50	-7.15	7p14.3
12	208734_x_at	RAB2	-1.45	2.19E-11	4.08E-08	-0.49	-7.14	8q12.1
13	201412_at	LRP10	-1.52	2.81E-11	4.36E-08	-0.48	-7.04	14q11.2
14	203535_at	S100A9	-2.26	5.52E-11	6.43E-08	-0.49	-7.03	1q21
15	201881_s_at	ARIH1	-1.42	3.25E-11	4.59E-08	-0.48	-7.02	15q24
16	227184_at		-2.35	5.43E-11	6.43E-08	-0.47	-6.91	
17	218107_at	FLJ21016	-1.44	7.37E-11	7.40E-08	-0.47	-6.90	1q42.12
18	223423_at	GPCR1	-1.98	7.55E-11	7.40E-08	-0.47	-6.90	3q26.2-q27
19	207269_at	DEFA4	-2.97	8.82E-11	8.15E-08	-0.47	-6.88	8p23
20	231644_at		-2.30	6.17E-11	6.77E-08	-0.46	-6.88	
21	231688_at		-3.55	9.19E-11	8.15E-08	-0.46	-6.82	
22	223993_s_at	HSPC163	-1.69	1.58E-10	1.28E-07	-0.47	-6.81	1q42.12
23	210951_x_at	RAB27A	-1.81	1.86E-10	1.38E-07	-0.47	-6.78	15q15-q21.1
24	201963_at	FACL2	-1.83	1.26E-10	1.07E-07	-0.46	-6.77	4q34-q35
25	208499_s_at	DNAJC3	-1.89	1.69E-10	1.31E-07	-0.46	-6.75	13q32
26	223664_x_at	BCL2L13	-1.30	2.89E-10	1.68E-07	-0.47	-6.71	22q11
27	244492_at		-1.81	2.03E-10	1.45E-07	-0.45	-6.68	

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
28	218077_s_at	ZDHHC3	-1.41	2.58E-10	1.68E-07	-0.46	-6.67	3p21.31
29	206177_s_at	ARG1	-3.56	2.26E-10	1.56E-07	-0.45	-6.67	6q23
30	225386_s_at	LOC92906	-2.40	2.71E-10	1.68E-07	-0.46	-6.67	2p22.2
31	202925_s_at	PLAGL2	-1.41	2.70E-10	1.68E-07	-0.46	-6.67	20q11.1
32	217739_s_at	PBEF	-1.80	2.98E-10	1.68E-07	-0.46	-6.66	7q22.1
33	210190_at	STX11	-2.40	2.95E-10	1.68E-07	-0.45	-6.62	6q24.1
34	218078_s_at	ZDHHC3	-1.36	3.43E-10	1.76E-07	-0.45	-6.61	3p21.31
35	202018_s_at	LTF	-3.33	3.20E-10	1.74E-07	-0.44	-6.60	3q21-q23
36	209514_s_at	RAB27A	-1.69	5.06E-10	2.36E-07	-0.46	-6.59	15q15-q21.1
37	203827_at	FLJ10055	-2.25	3.26E-10	1.74E-07	-0.44	-6.59	17q24.3
38	202197_at	MTMR3	-1.54	3.60E-10	1.76E-07	-0.44	-6.58	22q12.2
39	236760_at		-1.80	3.57E-10	1.76E-07	-0.44	-6.58	
40	205627_at	CDA	-3.37	4.41E-10	2.11E-07	-0.44	-6.53	1p36.2-p35
41	227621_at	WTAP	-1.56	6.11E-10	2.62E-07	-0.44	-6.52	6q25-q27
42	241692_at		-1.76	6.20E-10	2.62E-07	-0.44	-6.51	
43	213805_at	CGI-58	-1.70	5.57E-10	2.53E-07	-0.44	-6.50	3p25.3-p24.3
44	218217_at	RISC	-2.80	6.19E-10	2.62E-07	-0.44	-6.49	17q23.1
45	228685_at		-1.78	9.99E-10	3.72E-07	-0.45	-6.49	
46	236248_x_at		-2.27	6.57E-10	2.72E-07	-0.44	-6.49	
47	214246_x_at	MINK	-1.47	8.54E-10	3.39E-07	-0.44	-6.45	17p13.3
48	206174_s_at	PPP6C	-1.38	1.28E-09	4.10E-07	-0.45	-6.43	9q34.11
49	229699_at		-1.41	1.17E-09	3.88E-07	-0.44	-6.42	
50	209212_s_at	KLF5	-1.90	8.56E-10	3.39E-07	-0.43	-6.42	13q21.32

5.3 AML M2 versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	201193_at	IDH1	-2.05	2.59E-10	8.51E-06	-0.45	-6.64	2q33.3
2	207761_s_at	DKFZP586A0522	-1.58	1.29E-08	1.72E-04	-0.40	-5.93	12q13.12
3	208890_s_at	PLXNB2	-1.58	1.57E-08	1.72E-04	-0.41	-5.91	22q13.33
4	227007_at	LOC255104	-1.67	6.77E-08	4.15E-04	-0.38	-5.61	1p36.13
5	202395_at	NSF	-1.61	7.09E-08	4.15E-04	-0.38	-5.60	17q21
6	206488_s_at	CD36	-2.38	7.59E-08	4.15E-04	-0.38	-5.58	7q11.2
7	223950_s_at	DKFZp761A132	-1.43	1.51E-07	5.57E-04	-0.39	-5.51	16p13.3
8	229670_at		-1.86	1.20E-07	5.57E-04	-0.37	-5.48	
9	201889_at	FAM3C	-1.55	1.57E-07	5.57E-04	-0.37	-5.42	7q22.1-q31.1
10	224983_at		-1.40	1.87E-07	5.57E-04	-0.37	-5.41	
11	204168_at	MGST2	-1.53	1.83E-07	5.57E-04	-0.36	-5.40	4q28.3
12	213375_s_at	CG018	-1.60	2.07E-07	5.65E-04	-0.36	-5.36	13q12-q13
13	209189_at	FOS	-1.66	3.09E-07	6.76E-04	-0.37	-5.32	14q24.3
14	212685_s_at	TBL2	-1.47	2.91E-07	6.76E-04	-0.36	-5.31	7q11.23
15	228766_at		-2.64	2.99E-07	6.76E-04	-0.36	-5.29	
16	202570_s_at	KIAA0964	-1.68	3.55E-07	7.29E-04	-0.36	-5.27	20q11.22
17	52164_at	C11orf24	-1.43	4.41E-07	8.10E-04	-0.36	-5.23	11q13
18	228472_at		-1.83	4.97E-07	8.10E-04	-0.35	-5.20	

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
19	204112_s_at	HNMT	-2.56	4.74E-07	8.10E-04	-0.35	-5.20	2q21.3
20	204085_s_at	CLN5	-1.51	5.92E-07	8.10E-04	-0.36	-5.19	13q21.1-q32
21	212959_s_at	MGC4170	-1.46	4.90E-07	8.10E-04	-0.35	-5.19	12q23.3
22	218536_at	MRS2L	-1.39	5.56E-07	8.10E-04	-0.35	-5.18	6p22.3-p22.1
23	225882_at	YEA	-1.45	5.59E-07	8.10E-04	-0.35	-5.16	7q33
24	208370_s_at	DSCR1	-1.56	5.87E-07	8.10E-04	-0.35	-5.15	21q22.12
25	222581_at	XPR1	-1.53	7.05E-07	8.81E-04	-0.35	-5.13	1q25.1
26	203024_s_at	HTGN29	-1.36	7.80E-07	8.82E-04	-0.35	-5.12	5q31.1
27	202930_s_at	SUCLA2	-1.51	7.01E-07	8.81E-04	-0.35	-5.11	13q12.2-q13.3
28	217752_s_at	CN2	-1.54	7.25E-07	8.81E-04	-0.35	-5.11	18q22.3
29	201503_at	G3BP	-1.54	7.61E-07	8.82E-04	-0.34	-5.09	5q33.1
30	238440_at	CLYBL	-1.39	9.02E-07	9.87E-04	-0.35	-5.09	
31	204619_s_at	CSPG2	-2.93	1.03E-06	1.09E-03	-0.35	-5.04	5q14.3
32	224164_at	TPM3	1.65	2.18E-06	1.38E-03	0.40	5.04	1q21.2
33	202672_s_at	ATF3	-1.64	1.12E-06	1.15E-03	-0.34	-5.02	1q32.3
34	226262_at		-1.27	1.43E-06	1.17E-03	-0.35	-5.02	
35	212518_at	PIP5K1C	-1.31	1.39E-06	1.17E-03	-0.35	-5.00	19p13.3
36	217832_at	NSAP1	-1.38	1.25E-06	1.17E-03	-0.34	-4.99	6q14-q15
37	218967_s_at	PTER	-1.49	1.43E-06	1.17E-03	-0.34	-4.99	10p12
38	203429_s_at	C1orf9	1.48	2.50E-06	1.51E-03	0.38	4.98	1q24
39	214755_at	LOC91373	-1.43	1.40E-06	1.17E-03	-0.34	-4.98	9q34.3
40	218176_at	MAGEF1	-1.62	1.40E-06	1.17E-03	-0.34	-4.98	3q13
41	208865_at	CSNK1A1	-1.24	1.56E-06	1.22E-03	-0.34	-4.98	5q32
42	222637_at	PTD002	-1.66	1.46E-06	1.17E-03	-0.34	-4.97	5q22.3
43	204003_s_at	NLP_1	-1.49	1.44E-06	1.17E-03	-0.34	-4.97	7p15
44	218076_s_at	RICH1	-1.40	1.43E-06	1.17E-03	-0.33	-4.96	16p12.2
45	204646_at	DPYD	-1.80	1.75E-06	1.29E-03	-0.33	-4.92	1p22
46	218026_at	HSPC009	-1.47	1.93E-06	1.29E-03	-0.34	-4.91	17q21
47	235241_at	FLJ90709	-1.46	1.87E-06	1.29E-03	-0.33	-4.91	5q11.2
48	225712_at	GEMIN5	-1.56	1.88E-06	1.29E-03	-0.33	-4.91	5q33.2
49	222752_s_at	FLJ10874	-1.34	1.93E-06	1.29E-03	-0.33	-4.91	1q32.2
50	209616_s_at	CES1	-4.57	2.04E-06	1.31E-03	-0.34	-4.90	16q13-q22.1
5.4	AML M4 versus rest							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	202242_at	TM4SF2	-2.31	4.72E-09	1.82E-04	-0.42	-6.15	Xq11.4
2	222809_x_at	C14orf65	-1.77	1.74E-07	1.24E-03	-0.39	-5.51	14q32.31
3	227297_at		-2.33	1.23E-07	1.19E-03	-0.38	-5.50	
4	205330_at	MN1	-2.86	1.08E-07	1.19E-03	-0.37	-5.50	22q12.1
5	235824_at		-2.83	1.18E-07	1.19E-03	-0.37	-5.49	
6	231929_at		-4.56	1.93E-07	1.24E-03	-0.36	-5.38	
7	227108_at	STARD9	-1.54	4.54E-07	2.39E-03	-0.39	-5.35	15q14
8	204529_s_at	TOX	-2.04	5.57E-07	2.39E-03	-0.37	-5.23	8q11.23

9	206726_at	PGDS	-3.59	5.28E-07	2.39E-03	-0.36	-5.18	4q22.2
10	209153_s_at	TCF3	-1.60	1.70E-06	5.08E-03	-0.40	-5.18	19p13.3
11	211700_s_at	TRO	-3.04	7.79E-07	2.74E-03	-0.35	-5.11	Xp11.22-p11.21
12	209993_at	ABCB1	-2.11	7.78E-07	2.74E-03	-0.35	-5.10	7q21.1
13	218899_s_at	BAALC	-2.67	1.71E-06	5.08E-03	-0.34	-4.96	8q22.3
14	230896_at		-3.05	2.12E-06	5.86E-03	-0.35	-4.94	
15	215736_at		-1.74	4.19E-06	9.00E-03	-0.35	-4.84	
16	225645_at		-2.59	3.70E-06	8.41E-03	-0.34	-4.82	
17	219884_at	LHX6	-2.05	3.27E-06	8.36E-03	-0.33	-4.79	9q33.3
18	213187_x_at		1.23	1.33E-05	1.88E-02	0.42	4.79	
19	209994_s_at	ABCB1	-3.50	3.46E-06	8.36E-03	-0.32	-4.77	7q21.1
20	204352_at	TRAF5	-1.66	4.85E-06	9.86E-03	-0.34	-4.76	1q32
21	211343_s_at	COL13A1	-2.17	8.75E-06	1.66E-02	-0.35	-4.69	10q22
22	204078_at	SC65	-2.03	9.46E-06	1.66E-02	-0.34	-4.66	17q21.2
23	202576_s_at	FLJ11126	1.29	2.18E-05	2.33E-02	0.41	4.65	16q22.1
24	201360_at	CST3	1.95	3.42E-05	2.77E-02	0.45	4.60	20p11.21
25	205311_at	DDC	-1.84	1.54E-05	1.99E-02	-0.35	-4.60	7p11
26	226499_at		-1.40	1.07E-05	1.71E-02	-0.33	-4.58	
27	203913_s_at	HPGD	-2.91	9.32E-06	1.66E-02	-0.31	-4.56	4q34-q35
28	221078_s_at	FLJ10392	1.29	3.40E-05	2.77E-02	0.41	4.55	2p16.1
29	209583_s_at	MOX2	-2.30	1.01E-05	1.69E-02	-0.30	-4.52	3q12-q13
30	222842_at	AGO4	1.60	4.79E-05	3.27E-02	0.45	4.52	1p34.3
31	237865_x_at		-1.47	1.11E-05	1.71E-02	-0.31	-4.51	
32	207530_s_at	CDKN2B	-1.66	1.51E-05	1.99E-02	-0.32	-4.48	9p21
33	205383_s_at	ZNF288	-1.31	2.23E-05	2.33E-02	-0.34	-4.48	3q13.2
34	242064_at		-2.99	1.23E-05	1.83E-02	-0.30	-4.48	
35	211548_s_at	HPGD	-2.90	1.36E-05	1.88E-02	-0.30	-4.45	4q34-q35
36	226192_at	ANAPC7	-2.26	1.71E-05	2.07E-02	-0.30	-4.41	12q13.12
37	214930_at	KIAA0918	-2.98	1.67E-05	2.07E-02	-0.30	-4.40	13q31.1
38	222780_s_at	BAALC	-2.41	1.92E-05	2.25E-02	-0.30	-4.40	8q22.3
39	47560_at	FLJ11939	-1.54	2.66E-05	2.53E-02	-0.32	-4.39	19p13.12
40	210481_s_at	CD209L	-1.53	2.23E-05	2.33E-02	-0.31	-4.39	19p13
41	204717_s_at	SLC29A2	-1.71	2.69E-05	2.53E-02	-0.32	-4.38	11q13
42	216848_at	KIAA1660	-1.51	2.07E-05	2.33E-02	-0.30	-4.37	
43	228831_s_at	FLJ00058	-1.53	4.23E-05	3.12E-02	-0.34	-4.35	19p13.3
44	227923_at	SHANK3	-2.74	2.80E-05	2.58E-02	-0.31	-4.34	22q13.3
45	238127_at		-1.59	3.58E-05	2.82E-02	-0.32	-4.34	
46	219383_at	FLJ14213	-2.20	2.63E-05	2.53E-02	-0.30	-4.34	11p11.2
47	213725_x_at	LOC283824	-1.57	4.94E-05	3.27E-02	-0.35	-4.33	16p13.12
48	208227_x_at	ADAM22	-1.74	2.68E-05	2.53E-02	-0.30	-4.32	7q21
49	220817_at	TRPC4	-1.82	3.44E-05	2.77E-02	-0.31	-4.32	13q13.1-q13.2
50	219648_at	FLJ10116	-1.79	3.03E-05	2.66E-02	-0.30	-4.30	2q35
5.5	AML M5a versus rest							

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	201015_s_at	JUP	-7.69	7.18E-19	2.37E-14	-0.74	-10.60	17q21
2	205239_at	AREG	-4.58	2.26E-14	2.48E-10	-0.67	-9.32	4q13-q21
3	210665_at	TFPI	-5.05	1.67E-13	9.17E-10	-0.68	-9.24	2q31-q32.1
4	241769_at		-3.74	1.03E-15	1.69E-11	-0.60	-8.80	
5	225248_at	SPPL2B	-2.52	2.39E-11	7.17E-08	-0.65	-8.54	19p13.3
6	225233_at		-3.35	1.15E-13	7.57E-10	-0.57	-8.23	
7	212071_s_at	SPTBN1	-2.29	5.52E-09	5.87E-06	-0.67	-8.07	2p21
8	219686_at	HSA250839	-5.16	5.57E-14	4.59E-10	-0.54	-8.05	4p16.2
9	214953_s_at	APP	-3.13	5.72E-13	2.69E-09	-0.55	-7.92	21q21.3
10	227839_at	MBD5	-3.86	7.10E-10	1.22E-06	-0.61	-7.84	2q23.2
11	226442_at	ABTB1	-3.93	6.84E-13	2.82E-09	-0.52	-7.71	3q21
12	218778_x_at	EPS8R1	-2.25	3.47E-09	4.23E-06	-0.61	-7.69	19q13.42
13	200602_at	APP	-4.73	9.42E-11	2.32E-07	-0.56	-7.65	21q21.3
14	232438_at	EPS15R	-2.36	1.48E-10	3.25E-07	-0.55	-7.51	19p13.11
15	232618_at	CYorf15A	-4.78	1.48E-09	2.03E-06	-0.57	-7.42	Y
16	242028_at	FLJ38281	-1.98	1.59E-08	1.59E-05	-0.60	-7.39	19p13.13
17	212249_at	PIK3R1	-2.10	3.35E-09	4.23E-06	-0.57	-7.38	5q12-q13
18	212618_at	KIAA0295	-2.68	1.02E-11	3.73E-08	-0.50	-7.30	15q22.1
19	213541_s_at	ERG	-2.76	7.39E-07	4.00E-04	-0.71	-7.30	21q22.3
20	230541_at	LOC149134	-3.09	9.86E-11	2.32E-07	-0.51	-7.23	1q44
21	210664_s_at	TFPI	-3.74	1.21E-07	9.05E-05	-0.62	-7.17	2q31-q32.1
22	214627_at	EPX	-4.79	2.34E-11	7.17E-08	-0.48	-7.08	17q23.1
23	212013_at	D2S448	-9.90	3.46E-11	9.49E-08	-0.47	-6.98	2pter-p25.1
24	230805_at		-2.97	6.03E-08	4.85E-05	-0.56	-6.89	
25	223708_at	C1QTNF4	-5.79	1.25E-09	1.79E-06	-0.49	-6.82	11q11
26	239067_s_at	PANX2	-3.92	6.58E-10	1.22E-06	-0.48	-6.76	22q13.33
27	213056_at	KIAA1013	-2.13	2.82E-07	1.69E-04	-0.57	-6.71	3p14.1
28	226282_at		-11.36	1.72E-10	3.54E-07	-0.45	-6.71	
29	214966_at	GRIK5	-2.88	1.87E-06	8.22E-04	-0.63	-6.69	19q13.2
30	213258_at		-3.66	2.27E-06	9.22E-04	-0.62	-6.57	
31	212558_at	SPRY1	-2.90	2.27E-07	1.47E-04	-0.54	-6.57	4q27
32	217936_at		-1.95	3.74E-07	2.12E-04	-0.55	-6.54	
33	205910_s_at	CEL	-2.98	6.86E-10	1.22E-06	-0.44	-6.51	9q34.3
34	210487_at	DNTT	-40.05	7.40E-10	1.22E-06	-0.44	-6.45	10q23-q24
35	205048_s_at	PSPHL	-4.18	1.23E-09	1.79E-06	-0.44	-6.45	7q11.2
36	225436_at	LOC58489	-2.71	4.76E-08	3.92E-05	-0.49	-6.44	15q24.3
37	218935_at	EHD3	-2.67	8.54E-07	4.40E-04	-0.55	-6.41	2p21
38	207130_at	PRKCBP1	-2.35	6.68E-09	6.88E-06	-0.46	-6.41	20q13.12
39	206582_s_at	GPR56	-2.26	1.03E-09	1.62E-06	-0.43	-6.39	16q13
40	236198_at		-2.69	2.89E-07	1.70E-04	-0.52	-6.37	
41	213506_at	F2RL1	-5.41	4.23E-09	4.65E-06	-0.45	-6.36	5q13
42	203783_x_at	POLRMT	-2.56	1.93E-06	8.22E-04	-0.57	-6.35	19p13.3
43	235052_at	FLJ38451	-3.12	3.68E-06	1.30E-03	-0.60	-6.34	19q13.11
44	223714_at	ZNF256	-2.25	8.60E-06	2.51E-03	-0.65	-6.34	19q13.43

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
45	211534_x_at	PTPRN2	-2.06	2.68E-08	2.45E-05	-0.47	-6.34	7q36
46	226342_at		-3.51	8.69E-07	4.41E-04	-0.54	-6.32	
47	239251_at		-2.06	2.67E-06	1.02E-03	-0.58	-6.31	
48	212385_at		-3.04	2.67E-07	1.63E-04	-0.50	-6.30	
49	204529_s_at	TOX	-2.60	1.53E-07	1.05E-04	-0.49	-6.27	8q11.23
50	213891_s_at		-3.34	7.35E-08	5.77E-05	-0.48	-6.27	

5.6 AML M5b versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	200953_s_at	CCND2	-3.25	7.43E-23	5.24E-19	-0.98	-13.45	12p13
2	228402_at	MGC15435	-2.44	1.01E-23	9.50E-20	-0.87	-12.37	5q13.2
3	221004_s_at	ITM2C	-8.14	7.17E-26	2.03E-21	-0.81	-12.03	2q37
4	210664_s_at	TFPI	-5.54	3.65E-25	5.15E-21	-0.81	-11.96	2q31-q32.1
5	243364_at	AUTS2	-5.22	5.04E-20	1.02E-16	-0.85	-11.71	7q11.21
6	221731_x_at	CSPG2	4.51	5.62E-10	7.41E-08	1.35	11.23	5q14.3
7	204620_s_at	CSPG2	4.44	1.03E-09	1.26E-07	1.37	11.04	5q14.3
8	244740_at		-5.66	1.64E-22	9.24E-19	-0.75	-11.03	
9	210665_at	TFPI	-6.63	1.94E-21	6.85E-18	-0.75	-10.96	2q31-q32.1
10	200985_s_at	CD59	-3.24	1.89E-18	2.67E-15	-0.78	-10.81	11p13
11	209524_at	HDGFRP3	-13.13	5.15E-22	2.42E-18	-0.73	-10.80	15q11.2
12	235109_at		-6.31	3.32E-18	3.75E-15	-0.78	-10.78	
13	226676_at	EHZF	-12.82	1.24E-21	4.99E-18	-0.73	-10.72	18q11.1
14	235142_at	MGC17919	-4.49	1.55E-18	2.30E-15	-0.77	-10.71	1p34.3
15	202747_s_at	ITM2A	-4.83	1.18E-19	1.97E-16	-0.75	-10.67	Xq13.3-Xq21.2
16	202803_s_at	ITGB2	2.08	3.12E-10	4.57E-08	1.12	10.59	21q22.3
17	220403_s_at	P53AIP1	-3.72	2.46E-21	7.70E-18	-0.71	-10.57	11q24
18	228974_at		-2.87	2.62E-16	1.89E-13	-0.78	-10.52	
19	218086_at	NPDC1	-7.95	5.49E-21	1.55E-17	-0.70	-10.45	9q34.3
20	204158_s_at	TCIRG1	2.25	7.75E-10	9.77E-08	1.15	10.43	11q13.4-q13.5
21	226677_at	EHZF	-19.45	1.17E-20	2.75E-17	-0.71	-10.40	18q11.1
22	200602_at	APP	-7.88	1.04E-20	2.66E-17	-0.70	-10.36	21q21.3
23	228029_at	KIAA1982	-5.33	9.93E-20	1.75E-16	-0.71	-10.30	4p16.3
24	200665_s_at	SPARC	-5.40	1.59E-20	3.46E-17	-0.69	-10.30	5q31.3-q32
25	231982_at		-7.24	7.09E-14	2.74E-11	-0.82	-10.29	
26	201360_at	CST3	2.91	1.26E-09	1.44E-07	1.15	10.29	20p11.21
27	229256_at	FLJ32029	-2.00	7.08E-20	1.33E-16	-0.70	-10.26	11q13.3
28	201015_s_at	JUP	-7.14	2.42E-18	3.11E-15	-0.71	-10.20	17q21
29	202976_s_at	RHOBTB3	-3.44	7.71E-18	8.36E-15	-0.72	-10.16	5q14.3
30	233849_s_at	ARHGAP5	-4.10	5.39E-16	3.54E-13	-0.74	-10.09	14q12
31	244741_s_at		-3.32	1.86E-15	1.14E-12	-0.75	-10.06	
32	225308_s_at	KIAA1728	-4.66	3.15E-19	4.95E-16	-0.67	-9.91	2q24.2
33	238417_at	FLJ32029	-1.71	3.84E-13	1.23E-10	-0.79	-9.88	11q13.3
34	212463_at		-2.94	6.51E-17	5.56E-14	-0.70	-9.86	

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
35	213258_at		-3.75	2.27E-16	1.69E-13	-0.71	-9.85	
36	212599_at	AUTS2	-2.64	3.26E-18	3.75E-15	-0.68	-9.85	7q11.21
37	203973_s_at	CEBPD	2.53	1.77E-09	1.92E-07	1.07	9.84	8p11.2-p11.1
38	200871_s_at	PSAP	2.07	2.19E-09	2.27E-07	1.08	9.84	10q21-q22
39	244043_at		-4.26	1.53E-17	1.44E-14	-0.68	-9.76	
40	200951_s_at	CCND2	-3.54	2.26E-14	9.68E-12	-0.74	-9.76	12p13
41	204971_at	CSTA	2.42	3.00E-09	2.88E-07	1.06	9.64	3q21
42	217979_at	NET-6	-3.89	3.04E-17	2.68E-14	-0.67	-9.64	7p21.1
43	230460_at		-3.60	1.94E-16	1.52E-13	-0.68	-9.62	
44	218237_s_at	SLC38A1	-3.14	9.58E-15	4.36E-12	-0.71	-9.59	12q12
45	35820_at	GM2A	2.63	7.50E-09	6.21E-07	1.14	9.59	5q31.3-q33.1
46	209543_s_at	CD34	-5.44	2.28E-18	3.07E-15	-0.64	-9.58	1q32
47	216041_x_at	GRN	2.92	1.06E-08	8.45E-07	1.19	9.58	17q21.32
48	219922_s_at	LTBP3	-4.57	1.33E-17	1.34E-14	-0.66	-9.57	11q12
49	230664_at		-5.18	1.42E-17	1.39E-14	-0.65	-9.54	
50	215017_s_at	FLJ20275	-3.38	3.23E-16	2.23E-13	-0.68	-9.54	1p22.1

5.7 AML M6 versus rest

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211070_x_at	DBI	-3.10	4.27E-19	1.31E-15	-1.37	-17.49	2q12-q21
2	202428_x_at	DBI	-2.84	4.78E-17	5.85E-14	-1.36	-16.86	2q12-q21
3	201105_at	LGALS1	-11.02	2.29E-39	5.60E-35	-1.09	-16.26	22q13.1
4	224916_at		-3.30	2.05E-24	2.51E-20	-1.08	-14.99	
5	225605_at	LOC90313	-5.29	5.66E-18	1.38E-14	-1.15	-14.90	17q11.1
6	221928_at	LOC283445	-4.65	4.09E-21	2.00E-17	-0.97	-13.37	12q24.12
7	221666_s_at	ASC	-4.71	1.22E-16	1.36E-13	-1.02	-13.30	16p12-p11.2
8	235056_at		-2.55	2.43E-16	2.29E-13	-1.02	-13.25	
9	228209_at		-4.40	5.54E-13	2.19E-10	-1.08	-12.99	
10	220974_x_at	BA108L7.2	-4.61	9.57E-18	1.55E-14	-0.97	-12.95	10q24.31
11	235463_s_at	LOC253782	-2.24	1.56E-21	9.57E-18	-0.92	-12.84	2q31.1
12	224929_at		-2.60	1.01E-17	1.55E-14	-0.96	-12.81	
13	217226_s_at	BA108L7.2	-2.88	1.01E-17	1.55E-14	-0.96	-12.78	10q24.31
14	201037_at	PFKP	-2.99	8.37E-18	1.55E-14	-0.94	-12.57	10p15.3-p15.2
15	209389_x_at	DBI	-2.42	8.63E-11	1.68E-08	-1.08	-12.18	2q12-q21
16	213870_at	COL11A2	-3.29	4.51E-13	1.90E-10	-0.95	-11.82	6p21.3
17	214909_s_at	DDAH2	-3.15	4.54E-12	1.35E-09	-0.98	-11.79	6p21.3
18	224747_at	LOC92912	-1.83	1.42E-11	3.54E-09	-0.97	-11.60	15q23
19	201850_at	CAPG	-4.15	6.97E-24	5.69E-20	-0.79	-11.59	2cen-q24
20	228415_at	AP1S2	-2.26	1.03E-15	7.91E-13	-0.87	-11.52	Xp22.31
21	205081_at	CRIP1	-7.41	6.78E-18	1.38E-14	-0.83	-11.46	7q11.23
22	202262_x_at	DDAH2	-2.37	2.87E-11	6.63E-09	-0.96	-11.42	6p21.3
23	221581_s_at	WBSCR5	-2.77	1.96E-12	6.48E-10	-0.92	-11.38	7q11.23
24	58780_s_at	FLJ10357	-3.60	3.75E-15	2.48E-12	-0.86	-11.38	14q11.1

25	202659_at	PSMB10	-2.80	2.56E-11	5.97E-09	-0.93	-11.10	16q22.1
26	206674_at	FLT3	-4.60	1.91E-10	3.22E-08	-0.94	-10.95	13q12
27	224649_x_at	CFP1	-2.24	2.53E-11	5.97E-09	-0.91	-10.93	10p11.21
28	208983_s_at	PECAM1	-6.55	2.42E-20	8.47E-17	-0.76	-10.92	17q23
29	228678_at		-6.23	2.25E-17	3.07E-14	-0.79	-10.91	
30	209539_at	ARHGEF6	-2.00	4.83E-11	9.93E-09	-0.91	-10.86	Xq26
31	225214_at		-2.24	2.10E-16	2.15E-13	-0.79	-10.80	
32	205518_s_at	CMAH	-2.07	2.84E-15	1.99E-12	-0.80	-10.74	6p21.32
33	201487_at	CTSC	-2.40	4.76E-13	1.94E-10	-0.82	-10.56	11q14.1-q14.3
34	228595_at	HSD17B1	-3.40	4.34E-12	1.31E-09	-0.84	-10.53	17q11-q21
35	209983_s_at	NRXN2	-10.44	5.10E-21	2.08E-17	-0.70	-10.46	11q13
36	217286_s_at	NDRG3	-2.72	1.06E-09	1.44E-07	-0.92	-10.43	20q11.21-q11.23
37	225796_at		-1.91	4.04E-11	8.75E-09	-0.83	-10.19	
38	227268_at	LOC51136	-2.27	1.18E-10	2.16E-08	-0.84	-10.14	17q23.2
39	215537_x_at	DDAH2	-2.38	9.97E-11	1.89E-08	-0.83	-10.12	6p21.3
40	230161_at		-3.42	1.04E-10	1.94E-08	-0.83	-10.08	
41	243000_at		-3.48	·7.11E-14	3.51E-11	-0.75	-10.07	
42	1294_at	UBE1L	-1.98	2.80E-10	4.34E-08	-0.84	-10.06	3p21
43	231724_at	CRSP7	-4.05	6.68E-17	7.78E-14	-0.71	-10.04	19p13.11
44	226521_s_at	FLJ13614	-1.86	9.53E-11	1.84E-08	-0.82	-10.04	4q21.21-q21.23
45	206081_at	SLC24A1	-3.53	4.49E-13	1.90E-10	-0.76	-10.03	15q22
46	228242_at		-2.44	1.38E-09	1.80E-07	-0.87	-10.02	
47	221710_x_at	FLJ10647	-3.38	9.53E-10	1.32E-07	-0.86	-9.99	1p34.3
48	216015_s_at	CIAS1	-4.61	2.56E-13	1.18E-10	-0.75	-9.96	1q44
49	201613_s_at	RUVBL1	-2.63	6.75E-09	7.31E-07	-0.90	-9.96	3q21
50	221754_s_at	CORO1B	-5.31	1.19E-13	5.61E-11	-0.74	-9.94	11q13.1

Table 6

6. All-Pairs (AP)								
6.1	AML M0 versus AML M1							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	201069_at	MMP2	-6.94	1.45E-10	3.06E-06	-0.83	-7.42	16q13-q21
2	227889_at		-3.55	1.86E-10	3.06E-06	-0.82	-7.36	
3	209099_x_at	JAG1	-5.33	3.23E-10	3.53E-06	-0.80	-7.21	20p12.1-p11.23
4	235413_at	GGCX	-2.46	4.65E-09	2.18E-05	-0.84	-7.16	2p12
5	213110_s_at	COL4A5	-9.89	1.03E-09	6.90E-06	-0.81	-7.06	Xq22
6	216268_s_at	JAG1	-5.00	1.05E-09	6.90E-06	-0.77	-6.94	20p12.1-p11.23
7	242426_at	LOC145957	-3.68	2.66E-09	1.45E-05	-0.75	-6.74	15q23
8	225599_s_at		-2.46	1.07E-08	3.92E-05	-0.77	-6.68	

Table 5+6

9	219304_s_at	SCDGF-B	-3.25	9.40E-09	3.85E-05	-0.72	-6.43	11q22.3
10	223703_at	CDA017	-2.42	5.66E-08	1.24E-04	-0.74	-6.35	10q23.1
11	236738_at		-10.43	3.23E-08	1.06E-04	-0.70	-6.19	
12	209098_s_at	JAG1	-3.26	4.02E-08	1.13E-04	-0.68	-6.09	20p12.1-p11.23
13	236892_s_at		-7.33	5.02E-08	1.17E-04	-0.69	-6.08	
14	205366_s_at	HOXB6	-6.80	4.48E-08	1.13E-04	-0.68	-6.07	17q21.3
15	235749_at	UGCGL2	-3.96	4.50E-08	1.13E-04	-0.67	-6.07	13q32.1
16	242784_at		-1.77	6.10E-08	1.25E-04	-0.67	-6.01	
17	208967_s_at	AK2	-2.10	8.92E-08	1.72E-04	-0.67	-5.97	1p34
18	220416_at	KIAA1939	-2.83	2.68E-07	4.40E-04	-0.69	-5.92	15q15.3
19	225622_at	PAG	2.43	1.88E-05	6.55E-03	0.96	5.89	8q21.11
20	228542_at	MRS2L	-2.12	5.58E-07	7.62E-04	-0.70	-5.89	6p22.3-p22.1
21	225600_at		-1.83	2.29E-06	1.95E-03	-0.76	-5.89	
22	204215_at	MGC4175	1.80	9.37E-06	4.24E-03	0.86	5.88	7q21.1-q21.2
23	220162_s_at	CARD9	-2.55	7.93E-07	1.00E-03	-0.69	-5.78	9q34.3
24	235775_at	DKFZp762A217	-2.97	1.66E-07	3.01E-04	-0.65	-5.78	12q21.31
25	228904_at		-4.80	1.74E-07	3.01E-04	-0.64	-5.75	
26	202787_s_at	MAPKAPK3	-1.65	6.55E-07	8.59E-04	-0.65	-5.64	3p21.3
27	212820_at	RC3	-3.00	3.15E-07	4.69E-04	-0.62	-5.60	15q15.3
28	239791_at		-4.69	3.06E-07	4.69E-04	-0.62	-5.60	
29	201562_s_at	SORD	-1.60	2.37E-06	1.95E-03	-0.68	-5.57	15q15.3
30	232424_at	PRDM16	-7.26	4.06E-07	5.78E-04	-0.62	-5.53	1p36.23-p33
31	225603_s_at		-2.08	4.85E-06	2.74E-03	-0.69	-5.48	
32	205996_s_at	AK2	-1.85	2.47E-06	1.96E-03	-0.66	-5.48	1p34
33	201427_s_at	SEPP1	-3.37	2.99E-06	2.00E-03	-0.65	-5.43	5q31
34	230874_at		-1.93	3.84E-06	2.33E-03	-0.66	-5.42	
35	231897_at	LTB4DH	-2.07	9.04E-07	1.10E-03	-0.61	-5.41	9q32
36	202770_s_at	CCNG2	1.66	1.15E-05	4.70E-03	0.71	5.41	4q21.21
37	204565_at	HT012	-1.53	4.21E-06	2.46E-03	-0.66	-5.41	6p22.1
38	213217_at	ADCY2	-11.96	9.85E-07	1.15E-03	-0.64	-5.40	5p15.3
39	227716_at	SOC	-3.29	1.01E-06	1.15E-03	-0.59	-5.32	1p35.3
40	211367_s_at	CASP1	-2.05	2.17E-06	1.95E-03	-0.61	-5.28	11q23
41	224968_at	MGC15407	-1.55	2.02E-06	1.89E-03	-0.60	-5.27	2p16.1
42	229245_at	LOC149267	-3.28	1.38E-06	1.51E-03	-0.60	-5.27	1q32.1
43	209208_at	MPDU1	-3.06	1.70E-06	1.74E-03	-0.59	-5.26	17p13.1-p12
44	227492_at	OCLN	-2.26	1.50E-06	1.59E-03	-0.59	-5.25	5q13.1
45	200806_s_at	HSPD1	-2.04	2.57E-06	1.96E-03	-0.60	-5.21	2q33.1
46	225032_at	FAD104	-1.70	4.18E-06	2.46E-03	-0.61	-5.20	3q26.31
47	231736_x_at	MGST1	-2.64	1.67E-05	6.23E-03	-0.67	-5.18	12p12.3-p12.1
48	219080_s_at	CTPS2	-1.61	1.87E-05	6.55E-03	-0.68	-5.18	Xp22
49	242065_x_at	KIAA0982	1.44	5.15E-05	1.23E-02	0.77	5.17	10p15.3
50	212009_s_at	STIP1	-8.32	2.38E-06	1.95E-03	-0.61	-5.17	11q13

6.2	AML M0 versus AML M2							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	209099_x_at	JAG1	-8.56	1.47E-11	2.45E-07	-0.91	-8.01	20p12.1-p11.23
2	205653_at	CTSG	-7.05	1.28E-11	2.45E-07	-0.88	-7.92	14q11.2
3	202924_s_at	PLAGL2	-1.76	2.16E-11	2.45E-07	-0.86	-7.80	20q11.1
4	214575_s_at	AZU1	-7.96	2.84E-11	2.45E-07	-0.85	-7.72	19p13.3
5	218332_at	BEX1	-9.18	8.84E-11	6.10E-07	-0.84	-7.53	Xq21-q23
6	213110_s_at	COL4A5	-9.17	1.42E-10	8.17E-07	-0.85	-7.49	Xq22
7	216268_s_at	JAG1	-8.13	2.32E-10	1.00E-06	-0.84	-7.37	20p12.1-p11.23
8	206851_at	RNASE3	-5.17	2.20E-10	1.00E-06	-0.81	-7.32	14q24-q31
9	205633_s_at	ALAS1	-2.30	5.36E-10	2.06E-06	-0.78	-7.07	3p21.1
10	206871_at	ELA2	-4.56	4.38E-09	8.93E-06	-0.82	-7.06	19p13.3
11	214033_at	ABCC6	-2.49	3.19E-09	7.33E-06	-0.81	-7.05	16p13.1
12	242426_at	LOC145957	-3.72	8.82E-10	3.04E-06	-0.77	-6.98	15q23
13	220798_x_at	FLJ11535	-3.41	1.11E-08	1.82E-05	-0.81	-6.91	19p13.3
14	212820_at	RC3	-3.00	3.19E-09	7.33E-06	-0.77	-6.87	15q15.3
15	201444_s_at	ATP6IP2	-1.57	1.70E-09	4.59E-06	-0.76	-6.86	Xq21
16	202444_s_at	KEO4	-2.08	1.59E-09	4.59E-06	-0.76	-6.84	10q21-q22
17	231183_s_at	JAG1	-3.13	1.73E-09	4.59E-06	-0.75	-6.80	20p12.1-p11.23
18	235413_at	GGCX	-2.45	1.03E-08	1.78E-05	-0.78	-6.79	2p12
19	227716_at	SOC	-4.12	4.40E-09	8.93E-06	-0.74	-6.63	1p35.3
20	210254_at	MS4A3	-4.09	1.25E-08	1.96E-05	-0.75	-6.61	11q12
21	204214_s_at	RAB32	-2.11	5.04E-08	6.44E-05	-0.78	-6.57	6q24.2
22	205557_at	BPI	-5.59	6.23E-09	1.19E-05	-0.72	-6.52	20q11.23-q12
23	224973_at	C6orf37	-3.14	7.92E-09	1.44E-05	-0.71	-6.46	6q14
24	223703_at	CDA017	-2.35	8.24E-08	9.48E-05	-0.75	-6.39	10q23.1
25	227889_at		-2.99	2.27E-08	3.40E-05	-0.70	-6.29	
26	241985_at	FLJ37870	-2.17	1.27E-07	1.36E-04	-0.74	-6.28	5q13.3
27	214539_at	SERPINB10	-3.05	2.54E-08	3.65E-05	-0.68	-6.19	18q21.3
28	206157_at	PTX3	-3.78	4.67E-07	3.16E-04	-0.73	-6.07	3q25
29	206129_s_at	ARSB	-1.73	9.79E-07	4.83E-04	-0.76	-6.07	5p11-q13
30	219304_s_at	SCDGF-B	-2.37	6.17E-08	7.61E-05	-0.68	-6.06	11q22.3
31	203949_at	MPO	-3.75	8.36E-07	4.39E-04	-0.75	-6.04	17q23.1
32	228497_at	FLIPT1	-3.05	4.77E-08	6.44E-05	-0.67	-6.04	1p13.1
33	216667_at		-3.98	4.87E-08	6.44E-05	-0.67	-6.03	
34	206111_at	RNASE2	-2.77	2.22E-06	8.71E-04	-0.79	-6.03	14q24-q31
35	218865_at	FLJ22390	-9.74	8.15E-08	9.48E-05	-0.71	-6.03	1q42.11
36	227492_at	OCLN	-2.10	4.17E-07	3.08E-04	-0.70	-5.95	5q13.1
37	201858_s_at	PRG1	-1.88	3.66E-06	1.24E-03	-0.80	-5.95	10q22.1
38	208967_s_at	AK2	-1.92	2.56E-07	2.21E-04	-0.68	-5.89	1p34
39	203948_s_at	MPO	-4.49	6.21E-07	3.82E-04	-0.70	-5.89	17q23.1
40	225386_s_at	LOC92906	-3.10	1.26E-07	1.36E-04	-0.66	-5.87	2p22.2

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
41	235703_at		-2.45	1.24E-06	5.55E-04	-0.72	-5.87	
42	201118_at	PGD	-2.15	1.54E-07	1.51E-04	-0.65	-5.85	1p36.3-p36.13
43	225599_s_at		-2.51	1.48E-07	1.51E-04	-0.65	-5.82	
44	235749_at	UGCGL2	-4.63	1.30E-07	1.36E-04	-0.64	-5.80	13q32.1
45	217741_s_at	ZNF216	-1.77	2.01E-07	1.90E-04	-0.65	-5.77	9q13-q21
46	230874_at		-2.10	5.36E-07	3.49E-04	-0.67	-5.75	
47	204393_s_at	ACPP	-2.68	4.01E-07	3.07E-04	-0.66	-5.73	3q21-q23
48	201337_s_at	VAMP3	-1.88	2.41E-07	2.15E-04	-0.64	-5.73	1p36.22
49	209906_at	C3AR1	-4.77	2.04E-07	1.90E-04	-0.63	-5.70	12p13.31
50	210951_x_at	RAB27A	-2.24	8.36E-07	4.39E-04	-0.67	-5.70	15q15-q21.1

6.3   AML M0 versus AML M4

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	242963_at	MGC26963	-4.26	1.93E-11	6.35E-07	-1.23	-8.73	4q25
2	212820_at	RC3	-5.15	2.57E-10	2.83E-06	-1.17	-8.18	15q15.3
3	204971_at	CSTA	-5.05	2.09E-10	2.83E-06	-1.13	-8.03	3q21
4	235749_at	UGCGL2	-6.76	1.05E-09	6.91E-06	-1.13	-7.81	13q32.1
5	205382_s_at	DF	-5.79	5.16E-10	4.25E-06	-1.08	-7.72	19p13.3
6	205366_s_at	HOXB6	-13.07	3.72E-09	1.75E-05	-1.14	-7.61	17q21.3
7	238058_at		-2.45	3.19E-09	1.75E-05	-1.02	-7.24	
8	202924_s_at	PLAGL2	-2.00	8.03E-09	2.81E-05	-1.03	-7.16	20q11.1
9	227108_at	STARD9	2.55	1.48E-06	5.23E-04	1.27	7.12	15q14
10	205653_at	CTSG	-8.04	1.26E-08	3.12E-05	-1.04	-7.10	14q11.2
11	223703_at	CDA017	-3.36	6.33E-09	2.61E-05	-0.99	-7.06	10q23.1
12	236892_s_at		-10.03	2.54E-08	4.00E-05	-1.04	-6.98	
13	208702_x_at	APLP2	-2.61	8.52E-09	2.81E-05	-0.97	-6.93	11q24
14	228904_at		-5.84	2.25E-08	4.00E-05	-0.99	-6.87	
15	201943_s_at	CPD	-2.95	1.32E-08	3.12E-05	-0.97	-6.86	17p11.1-q11.2
16	205600_x_at	HOXB5	-2.06	1.13E-08	3.12E-05	-0.96	-6.86	17q21.3
17	208223_s_at	ACVR1B	-2.17	1.17E-08	3.12E-05	-0.96	-6.84	12q13
18	201444_s_at	ATP6IP2	-1.80	2.50E-08	4.00E-05	-0.97	-6.77	Xq21
19	214033_at	ABCC6	-2.98	1.70E-08	3.50E-05	-0.95	-6.76	16p13.1
20	219304_s_at	SCDGF-B	-3.25	2.50E-08	4.00E-05	-0.96	-6.74	11q22.3
21	205601_s_at	HOXB5	-2.58	1.69E-08	3.50E-05	-0.94	-6.74	17q21.3
22	214575_s_at	AZU1	-7.48	2.42E-08	4.00E-05	-0.95	-6.72	19p13.3
23	239791_at		-7.05	5.79E-08	6.59E-05	-0.98	-6.65	
24	201940_at	CPD	-2.62	2.68E-08	4.02E-05	-0.93	-6.64	17p11.1-q11.2
25	216268_s_at	JAG1	-6.76	6.80E-08	7.24E-05	-0.98	-6.64	20p12.1-p11.23
26	227038_at	MGC26963	-6.40	3.22E-08	4.43E-05	-0.94	-6.62	4q25
27	204779_s_at	HOXB7	-3.91	7.76E-08	8.00E-05	-0.98	-6.61	17q21.3
28	200886_s_at	PGAM1	-2.14	3.79E-08	4.90E-05	-0.93	-6.59	10q25.3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
29	214875_x_at	APLP2	-2.72	2.96E-08	4.25E-05	-0.92	-6.59	11q24
30	209099_x_at	JAG1	-7.12	9.13E-08	8.86E-05	-0.98	-6.56	20p12.1-p11.23
31	227716_at	SOC	-7.69	1.21E-07	1.14E-04	-1.01	-6.56	1p35.3
32	217995_at	SQRDL	-2.16	3.88E-08	4.90E-05	-0.92	-6.55	15q15
33	201360_at	CST3	-3.83	4.01E-08	4.90E-05	-0.91	-6.51	20p11.21
34	211404_s_at	APLP2	-2.36	5.20E-08	6.12E-05	-0.91	-6.49	11q24
35	203676_at	GNS	-4.01	8.33E-08	8.33E-05	-0.92	-6.42	12q14
36	213110_s_at	COL4A5	-9.23	1.92E-07	1.41E-04	-0.97	-6.37	Xq22
37	223718_at	ACRBP	-3.19	6.46E-08	7.11E-05	-0.89	-6.37	12p13.31
38	207270_x_at	CMRF35	-3.52	1.91E-07	1.41E-04	-0.91	-6.26	17q25.2
39	206111_at	RNASE2	-3.07	3.48E-07	1.97E-04	-0.90	-6.22	14q24-q31
40	203834_s_at	TGOLN2	-1.78	1.81E-07	1.41E-04	-0.88	-6.21	2p11.2
41	218404_at	SNX10	-2.67	1.73E-07	1.41E-04	-0.88	-6.19	7p15.2
42	211004_s_at	ALDH3B1	-2.06	1.66E-07	1.41E-04	-0.88	-6.18	11q13
43	235413_at	GGCX	-2.76	1.30E-07	1.19E-04	-0.87	-6.17	2p12
44	33197_at	MYO7A	-2.14	1.38E-07	1.23E-04	-0.86	-6.16	11q13.5
45	235521_at	HOXA3	-4.37	1.70E-07	1.41E-04	-0.87	-6.13	7p15-p14
46	213622_at	COL9A2	-2.63	1.89E-07	1.41E-04	-0.86	-6.11	1p33-p32
47	222503_s_at	FLJ10904	-1.78	3.25E-07	1.94E-04	-0.87	-6.09	5q13.2
48	223017_at	TLP19	-1.56	2.19E-07	1.54E-04	-0.86	-6.09	1p32.3
49	200654_at	P4HB	-1.83	2.91E-07	1.82E-04	-0.86	-6.08	17q25
50	201337_s_at	VAMP3	-2.19	2.00E-07	1.43E-04	-0.86	-6.08	1p36.22

6.4 AML M0 versus AML M5a

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	220981_x_at	NXF2	-2.47	8.97E-07	2.43E-02	-1.29	-6.58	Xq22-q23
2	242051_at		3.95	2.54E-06	3.25E-02	1.31	6.49	
3	201015_s_at	JUP	17.77	2.31E-05	4.97E-02	1.45	6.14	17q21
4	226602_s_at		2.25	3.60E-06	3.25E-02	1.20	6.08	
5	207675_x_at	ARTN	-2.36	6.11E-05	6.66E-02	-1.39	-6.01	1p33-p32
6	213541_s_at	ERG	4.09	2.32E-05	4.97E-02	1.16	5.62	21q22.3
7	235749_at	UGCGL2	-6.75	1.60E-04	7.14E-02	-1.36	-5.58	13q32.1
8	225775_at		2.56	1.88E-05	4.97E-02	1.12	5.55	
9	220798_x_at	FLJ11535	-3.15	1.76E-05	4.97E-02	-1.10	-5.52	19p13.3
10	212535_at	MEF2A	3.21	3.96E-05	6.31E-02	1.16	5.49	15q26
11	202001_s_at	NDUFA6	-1.77	7.29E-05	6.66E-02	-1.18	-5.48	22q13.2-q13.31
12	205382_s_at	DF	-4.66	4.62E-05	6.35E-02	-1.14	-5.47	19p13.3
13	220924_s_at	SLC38A2	1.71	1.58E-05	4.97E-02	1.08	5.46	12q
14	231561_s_at	APOC2	-2.04	2.35E-05	4.97E-02	-1.08	-5.41	19q13.2
15	218928_s_at	SLC37A1	3.14	1.89E-05	4.97E-02	1.07	5.40	21q22.3
16	224252_s_at	FXYD5	1.93	2.09E-05	4.97E-02	1.07	5.39	19q12-q13.1
17	218825_at	ZNEU1	4.76	1.97E-05	4.97E-02	1.06	5.37	9q34.3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
18	206265_s_at	GPLD1	-3.33	5.13E-05	6.50E-02	-1.09	-5.31	6p22.3-p22.2
19	212249_at	PIK3R1	3.42	8.14E-05	6.66E-02	1.17	5.30	5q12-q13
20	231431_s_at		2.09	6.79E-05	6.66E-02	1.13	5.27	
21	218312_s_at	FLJ12895	2.74	2.38E-05	4.97E-02	1.03	5.25	19q13.43
22	218041_x_at	SLC38A2	1.64	2.88E-05	5.21E-02	1.03	5.21	12q
23	219789_at	NPR3	5.54	5.28E-05	6.50E-02	1.07	5.21	5p14-p13
24	221004_s_at	ITM2C	5.27	9.88E-05	6.66E-02	1.16	5.20	2q37
25	204529_s_at	TOX	6.77	1.16E-04	6.69E-02	1.20	5.20	8q11.23
26	219991_at	SLC2A9	-2.27	1.26E-04	6.76E-02	-1.11	-5.17	4p16-p15.3
27	215111_s_at	TSC22	3.55	2.72E-05	5.21E-02	1.01	5.17	13q14
28	206240_s_at	ZNF136	1.77	3.87E-05	6.31E-02	1.02	5.14	19p13.2-p13.12
29	202551_s_at	CRIM1	9.22	1.16E-04	6.69E-02	1.15	5.13	2p21
30	212071_s_at	SPTBN1	4.15	1.27E-04	6.76E-02	1.15	5.10	2p21
31	242028_at	FLJ38281	2.49	8.59E-05	6.66E-02	1.07	5.09	19p13.13
32	200654_at	P4HB	-1.87	8.42E-05	6.66E-02	-1.04	-5.07	17q25
33	222362_at	IRS3L	-2.93	1.04E-04	6.66E-02	-1.05	-5.07	7q22
34	200827_at	PLOD	-2.58	9.77E-05	6.66E-02	-1.05	-5.07	1p36.3-p36.2
35	201859_at	PRG1	-1.57	4.69E-05	6.35E-02	-1.00	-5.05	10q22.1
36	205741_s_at	DTNA	-2.11	2.94E-04	8.61E-02	-1.15	-5.01	18q12
37	219054_at	FLJ14054	6.35	8.38E-05	6.66E-02	1.02	4.98	5p13.3
38	235199_at		2.30	4.57E-05	6.35E-02	0.98	4.97	
39	218801_at	UGCGL2	-4.01	2.85E-04	8.59E-02	-1.12	-4.96	13q32.1
40	216689_x_at	ARHGAP1	-1.45	8.96E-05	6.66E-02	-1.01	-4.96	11p12-q12
41	213147_at	HOXA10	-2.06	6.12E-05	6.66E-02	-0.98	-4.93	7p15-p14
42	58900_at	LOC222070	-1.42	7.50E-05	6.66E-02	-0.98	-4.93	7p13
43	209706_at	NKX3-1	-2.81	1.51E-04	7.14E-02	-1.02	-4.91	8p21
44	232406_at		-2.36	9.86E-05	6.66E-02	-0.99	-4.90	
45	204971_at	CSTA	-4.72	2.49E-04	8.05E-02	-1.07	-4.89	3q21
46	226018_at	Ells1	3.73	1.79E-04	7.25E-02	1.08	4.88	7p15.1
47	203768_s_at	STS	-2.30	1.68E-04	7.14E-02	-1.02	-4.88	Xp22.32
48	215622_x_at	PHF7	-1.46	6.16E-05	6.66E-02	-0.96	-4.87	3p21.31
49	201858_s_at	PRG1	-1.93	7.53E-05	6.66E-02	-0.96	-4.84	10q22.1
50	201029_s_at	CD99	1.80	7.52E-05	6.66E-02	0.94	4.78	Xp22.32
6.5	AML M0 versus AML M5b							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	221731_x_at	CSPG2	-12.07	3.52E-11	1.36E-07	-2.57	-13.20	5q14.3
2	204620_s_at	CSPG2	-11.01	5.86E-11	1.86E-07	-2.50	-12.84	5q14.3
3	204971_at	CSTA	-7.66	5.03E-13	1.36E-08	-2.25	-12.58	3q21
4	201360_at	CST3	-5.75	5.82E-12	3.93E-08	-2.13	-11.80	20p11.21
5	205382_s_at	DF	-7.95	5.31E-12	3.93E-08	-2.07	-11.55	19p13.3
6	216041_x_at	GRN	-5.67	8.25E-11	1.86E-07	-2.10	-11.31	17q21.32

7	200678_x_at	GRN	-5.44	8.08E-11	1.86E-07	-2.09	-11.26	17q21.32
8	202803_s_at	ITGB2	-3.10	3.28E-12	3.93E-08	-1.98	-11.18	21q22.3
9	218217_at	RISC	-7.82	1.10E-09	1.35E-06	-2.20	-11.11	17q23.1
10	204158_s_at	TCIRG1	-2.93	1.41E-11	7.60E-08	-1.96	-10.96	11q13.4-q13.5
11	205601_s_at	HOXB5	-3.77	7.84E-11	1.86E-07	-1.93	-10.65	17q21.3
12	211284_s_at	GRN	-6.33	7.15E-10	9.66E-07	-2.02	-10.61	17q21.32
13	200886_s_at	PGAM1	-2.94	2.15E-11	9.69E-08	-1.88	-10.56	10q25.3
14	213622_at	COL9A2	-3.30	6.74E-11	1.86E-07	-1.90	-10.54	1p33-p32
15	217728_at	S100A6	-4.10	5.63E-10	8.01E-07	-1.87	-10.14	1q21
16	205366_s_at	HOXB6	-17.89	1.20E-08	8.98E-06	-2.10	-10.07	17q21.3
17	205786_s_at	ITGAM	-4.13	1.07E-10	2.22E-07	-1.74	-9.81	16p11.2
18	211404_s_at	APLP2	-3.51	3.55E-10	5.32E-07	-1.77	-9.79	11q24
19	203574_at	NFIL3	-2.76	1.17E-10	2.26E-07	-1.73	-9.74	9q22
20	215075_s_at	GRB2	-2.21	1.04E-09	1.34E-06	-1.74	-9.53	17q24-q25
21	200871_s_at	PSAP	-2.64	1.56E-10	2.81E-07	-1.68	-9.49	10q21-q22
22	202363_at	SPOCK	-2.96	1.97E-10	3.32E-07	-1.68	-9.47	5q31
23	35820_at	GM2A	-3.58	2.91E-10	4.62E-07	-1.67	-9.41	5q31.3-q33.1
24	208438_s_at	FGR	-6.69	9.67E-09	7.69E-06	-1.80	-9.34	1p36.2-p36.1
25	209166_s_at	MAN2B1	-2.77	2.45E-09	2.88E-06	-1.72	-9.33	19cen-q13.1
26	212807_s_at	SORT1	-5.63	8.14E-09	7.32E-06	-1.71	-9.08	1p21.3-p13.1
27	208702_x_at	APLP2	-3.68	9.19E-09	7.69E-06	-1.67	-8.91	11q24
28	226276_at	LOC153339	-3.19	9.68E-09	7.69E-06	-1.65	-8.83	5q14.1
29	202877_s_at	C1QR1	-4.20	1.45E-08	9.53E-06	-1.62	-8.68	20p11.21
30	225373_at	PP2135	-4.08	3.75E-08	1.63E-05	-1.68	-8.68	10q22.3
31	243296_at	PBEF	-4.32	1.55E-08	9.70E-06	-1.62	-8.65	7q22.1
32	224818_at		-6.47	2.90E-08	1.43E-05	-1.65	-8.64	
33	210549_s_at	CCL23	-13.85	8.07E-08	2.54E-05	-1.75	-8.64	17q12
34	205600_x_at	HOXB5	-2.55	7.67E-09	7.14E-06	-1.56	-8.56	17q21.3
35	204647_at	HOMER3	-7.92	8.59E-08	2.58E-05	-1.70	-8.50	19p13.11
36	206278_at	PTAFR	-9.29	1.58E-07	3.59E-05	-1.78	-8.48	1p35-p34.3
37	218559_s_at	MAFB	-11.01	5.72E-08	2.11E-05	-1.64	-8.44	20q11.2-q13.1
38	212737_at	GM2A	-3.20	6.76E-09	6.81E-06	-1.51	-8.38	5q31.3-q33.1
39	211429_s_at	SERPINA1	-12.67	1.82E-07	4.02E-05	-1.76	-8.38	14q32.1
40	228904_at		-6.98	8.04E-08	2.54E-05	-1.63	-8.34	
41	211416_x_at	GGTLA4	-2.42	2.43E-08	1.34E-05	-1.55	-8.32	20p11.1
42	200798_x_at	MCL1	-2.26	6.81E-09	6.81E-06	-1.49	-8.31	1q21
43	203555_at	PTPN18	-3.65	2.64E-08	1.38E-05	-1.53	-8.27	2q21.1
44	202096_s_at	BZRP	-3.36	1.43E-08	9.53E-06	-1.49	-8.22	22q13.31
45	225372_at	PP2135	-5.61	1.96E-07	4.18E-05	-1.68	-8.21	10q22.3
46	200742_s_at	CLN2	-2.72	1.83E-08	1.12E-05	-1.50	-8.21	11p15
47	217521_at	HAL	-3.89	1.00E-08	7.73E-06	-1.47	-8.18	12q22-q24.1
48	219358_s_at	CENTA2	-3.20	1.12E-07	2.88E-05	-1.60	-8.17	17q11.2

49	232617_at	CTSS	-3.78	2.69E-08	1.38E-05	-1.49	-8.11	1q21
50	201858_s_at	PRG1	-2.28	1.48E-08	9.53E-06	-1.46	-8.09	10q22.1

6.6	AML M0 versus AML M6							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	218223_s_at	CKIP-1	3.76	2.79E-07	4.70E-03	1.53	7.44	1q21.2
2	201029_s_at	CD99	2.21	5.66E-07	4.70E-03	1.52	7.30	Xp22.32
3	209619_at	CD74	3.08	3.79E-07	4.70E-03	1.46	7.13	5q32
4	201037_at	PFKP	3.59	2.49E-06	1.02E-02	1.57	7.11	10p15.3-p15.2
5	209321_s_at	ADCY3	2.66	1.07E-06	5.94E-03	1.49	7.09	2p24-p22
6	226602_s_at		2.62	6.74E-07	4.70E-03	1.45	7.04	
7	214909_s_at	DDAH2	3.86	3.68E-06	1.14E-02	1.46	6.72	6p21.3
8	231280_at		-3.56	1.84E-05	1.88E-02	-1.47	-6.60	
9	206871_at	ELA2	-4.96	7.67E-06	1.50E-02	-1.41	-6.57	19p13.3
10	238752_at		-3.06	4.07E-05	2.52E-02	-1.49	-6.45	
11	242051_at		3.45	5.21E-06	1.27E-02	1.38	6.45	
12	202262_x_at	DDAH2	2.89	7.48E-06	1.50E-02	1.39	6.38	6p21.3
13	224252_s_at	FXYD5	2.04	2.71E-06	1.02E-02	1.30	6.35	19q12-q13.1
14	202332_at	CSNK1E	3.01	2.93E-06	1.02E-02	1.30	6.33	22q13.1
15	213262_at	SACS	3.12	1.08E-05	1.62E-02	1.29	6.06	13q12
16	209876_at	GIT2	2.79	4.76E-06	1.27E-02	1.24	6.04	12q24.1
17	219858_s_at	FLJ20160	2.58	5.46E-06	1.27E-02	1.24	6.04	2q32.3
18	213072_at	LOC157542	-2.02	6.27E-05	3.17E-02	-1.35	-5.98	8q24.3
19	235056_at		2.64	1.96E-05	1.88E-02	1.30	5.94	
20	201862_s_at	LRRFIP1	2.14	8.58E-06	1.50E-02	1.21	5.87	2q37.3
21	218928_s_at	SLC37A1	3.66	8.14E-06	1.50E-02	1.20	5.85	21q22.3
22	213725_x_at	LOC283824	3.43	2.67E-05	2.21E-02	1.29	5.83	16p13.12
23	209320_at	ADCY3	2.02	1.87E-05	1.88E-02	1.23	5.77	2p24-p22
24	221004_s_at	ITM2C	8.79	4.06E-05	2.52E-02	1.34	5.76	2q37
25	215537_x_at	DDAH2	3.08	2.89E-05	2.21E-02	1.26	5.74	6p21.3
26	209301_at	CA2	-3.88	7.16E-05	3.28E-02	-1.27	-5.71	8q22
27	206093_x_at	TNXB	-7.53	3.74E-04	4.40E-02	-1.59	-5.70	6p21.3
28	201858_s_at	PRG1	-1.87	1.10E-05	1.62E-02	-1.17	-5.69	10q22.1
29	225605_at	LOC90313	7.08	4.44E-05	2.62E-02	1.31	5.69	17q11.1
30	210987_x_at		-3.57	1.50E-04	3.72E-02	-1.33	-5.67	
31	209431_s_at	ZNF278	2.59	1.07E-05	1.62E-02	1.16	5.66	22q12.2
32	221485_at	B4GALT5	-2.48	2.33E-05	2.17E-02	-1.18	-5.66	20q13.1-q13.2
33	226143_at	RAI1	1.64	1.27E-05	1.69E-02	1.16	5.64	17p11.2
34	221791_s_at	HSPC016	-1.25	1.60E-05	1.88E-02	-1.16	-5.64	3p21.31
35	206177_s_at	ARG1	-3.40	1.40E-05	1.78E-02	-1.16	-5.64	6q23
36	201859_at	PRG1	-1.52	1.25E-05	1.69E-02	-1.14	-5.60	10q22.1
37	222022_at		-2.31	5.38E-05	2.90E-02	-1.21	-5.60	

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
38	201561_s_at	CLSTN1	2.79	3.10E-05	2.21E-02	1.20	5.59	1p36.22
39	244427_at	KIF23	-2.23	3.99E-05	2.52E-02	-1.18	-5.57	15q22.31
40	207957_s_at	PRKCB1	3.00	1.79E-05	1.88E-02	1.14	5.54	16p11.2
41	218084_x_at	FXYD5	1.76	4.52E-05	2.62E-02	1.18	5.54	19q12-q13.1
42	208754_s_at	NAP1L1	2.18	1.95E-05	1.88E-02	1.14	5.53	12q21.1
43	235199_at		2.52	1.83E-05	1.88E-02	1.11	5.44	
44	225045_at	FLJ10392	4.29	2.83E-05	2.21E-02	1.14	5.44	2p16.1
45	216705_s_at	ADA	4.48	5.88E-05	3.03E-02	1.21	5.42	20q12-q13.11
46	230037_at	CD8B1	-2.12	5.36E-05	2.90E-02	-1.15	-5.41	2p12
47	91920_at	BCAN	-1.66	8.34E-05	3.34E-02	-1.17	-5.40	1q31
48	228443_s_at	SET07	-1.58	1.76E-04	3.83E-02	-1.22	-5.35	13q11-q13
49	223754_at	MGC13057	-4.91	4.10E-04	4.47E-02	-1.34	-5.33	2q32.3
50	202769_at	CCNG2	2.15	2.85E-05	2.21E-02	1.10	5.32	4q21.21

6.7 AML M1 versus AML M2

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	202917_s_at	S100A8	-1.85	3.00E-11	6.19E-07	-0.63	-7.27	1q21
2	205033_s_at	DEFA1	-2.40	4.47E-10	4.62E-06	-0.60	-6.83	8p23.2-p23.1
3	207269_at	DEFA4	-3.54	1.48E-09	1.02E-05	-0.59	-6.61	8p23
4	223423_at	GPCR1	-2.28	3.46E-09	1.79E-05	-0.58	-6.46	3q26.2-q27
5	202018_s_at	LTF	-4.41	1.31E-08	5.42E-05	-0.59	-6.27	3q21-q23
6	231688_at		-4.88	2.95E-08	9.21E-05	-0.60	-6.16	
7	206676_at	CEACAM8	-5.12	3.12E-08	9.21E-05	-0.61	-6.15	19q13.2
8	205557_at	BPI	-3.77	4.81E-08	1.10E-04	-0.54	-5.92	20q11.23-q12
9	220643_s_at	FAIM	1.87	6.20E-08	1.28E-04	0.55	5.90	3q22.3
10	203535_at	S100A9	-2.36	4.05E-08	1.05E-04	-0.52	-5.87	1q21
11	206177_s_at	ARG1	-5.01	1.71E-07	1.86E-04	-0.59	-5.78	6q23
12	228378_at	DKFZp434N2030	-1.68	8.85E-08	1.45E-04	-0.52	-5.75	12q21.33
13	202925_s_at	PLAGL2	-1.50	1.02E-07	1.45E-04	-0.52	-5.73	20q11.1
14	222753_s_at	FLJ22649	-1.43	1.04E-07	1.45E-04	-0.51	-5.71	4q34.2
15	210140_at	CST7	-2.31	1.05E-07	1.45E-04	-0.51	-5.70	20p11.21
16	206861_s_at	CGGBP1	-1.28	1.01E-07	1.45E-04	-0.50	-5.68	3p12-p11.1
17	210951_x_at	RAB27A	-1.87	1.25E-07	1.52E-04	-0.50	-5.63	15q15-q21.1
18	209212_s_at	KLF5	-2.18	2.41E-07	2.26E-04	-0.54	-5.63	13q21.32
19	203429_s_at	C1orf9	-1.68	1.20E-07	1.52E-04	-0.49	-5.63	1q24
20	204351_at	S100P	-3.18	1.48E-07	1.70E-04	-0.50	-5.61	4p16
21	211657_at	CEACAM6	-3.88	2.92E-07	2.51E-04	-0.54	-5.60	19q13.2
22	204218_at	DKFZP564M082	-1.34	2.12E-07	2.18E-04	-0.50	-5.55	11q13.2
23	213805_at	CGI-58	-1.87	3.20E-07	2.56E-04	-0.51	-5.52	3p25.3-p24.3
24	208361_s_at	BN51T	1.65	2.22E-07	2.18E-04	0.48	5.50	8q21
25	244756_at		-1.65	3.22E-07	2.56E-04	-0.49	-5.47	

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
26	218332_at	BEX1	-3.21	3.69E-07	2.82E-04	-0.50	-5.46	Xq21-q23
27	223584_s_at	DKFZP566C134	-1.62	2.73E-07	2.45E-04	-0.47	-5.43	7p14.3
28	207329_at	MMP8	-5.78	7.73E-07	3.48E-04	-0.57	-5.43	11q22.3
29	203757_s_at	CEACAM6	-4.35	7.29E-07	3.48E-04	-0.53	-5.39	19q13.2
30	230111_at		-2.74	7.70E-07	3.48E-04	-0.54	-5.39	
31	209211_at	KLF5	-2.47	6.60E-07	3.48E-04	-0.51	-5.38	13q21.32
32	202468_s_at	CTNNAL1	-1.75	4.26E-07	3.15E-04	-0.47	-5.35	9q31.2
33	206871_at	ELA2	-2.17	4.72E-07	3.25E-04	-0.47	-5.32	19p13.3
34	202166_s_at	PPP1R2	-1.39	4.63E-07	3.25E-04	-0.46	-5.32	3q29
35	218640_s_at	FLJ13187	-1.56	6.28E-07	3.48E-04	-0.48	-5.32	8q22.1
36	208723_at	USP11	1.54	6.31E-07	3.48E-04	0.48	5.30	Xp11.23
37	227309_at		-1.78	6.84E-07	3.48E-04	-0.47	-5.28	
38	224759_s_at	MGC17943	1.77	7.71E-07	3.48E-04	0.48	5.27	12q24.11
39	228084_at		1.73	6.95E-07	3.48E-04	0.47	5.26	
40	209514_s_at	RAB27A	-1.71	6.61E-07	3.48E-04	-0.46	-5.26	15q15-q21.1
41	202130_at	SUDD	-1.61	6.93E-07	3.48E-04	-0.47	-5.26	18q11.2
42	225475_at	MI-ER1	-1.46	6.29E-07	3.48E-04	-0.46	-5.26	1p31.2
43	227274_at	SYNJ2BP	1.57	7.03E-07	3.48E-04	0.46	5.23	14q24.1
44	208499_s_at	DNAJC3	-1.83	7.60E-07	3.48E-04	-0.46	-5.23	13q32
45	204370_at	HEAB	-1.44	7.70E-07	3.48E-04	-0.46	-5.22	11q12
46	204776_at	THBS4	-1.76	8.22E-07	3.61E-04	-0.46	-5.21	5q13
47	200998_s_at	CKAP4	-2.16	1.09E-06	4.25E-04	-0.48	-5.21	12q24.11
48	209939_x_at	CFLAR	-1.65	9.79E-07	4.09E-04	-0.47	-5.20	2q33-q34
49	211275_s_at	GYG	-1.69	1.03E-06	4.09E-04	-0.47	-5.20	3q24-q25.1
50	225498_at	C20orf178	-1.40	7.74E-07	3.48E-04	-0.45	-5.19	20q11.21

6.8   AML M1 versus AML M4

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	213187_x_at		-1.37	3.50E-08	6.17E-04	-0.63	-6.14	
2	223993_s_at	HSPC163	-1.99	1.13E-07	8.52E-04	-0.67	-6.10	1q42.12
3	204352_at	TRAF5	2.28	4.11E-08	6.17E-04	0.61	6.00	1q32
4	208734_x_at	RAB2	-1.50	1.10E-07	8.52E-04	-0.64	-5.99	8q12.1
5	209249_s_at	GHITM	-1.31	2.89E-07	9.12E-04	-0.61	-5.74	10q23.1
6	201963_at	FACL2	-1.91	4.25E-07	9.12E-04	-0.62	-5.72	4q34-q35
7	204971_at	CSTA	-2.22	2.80E-07	9.12E-04	-0.60	-5.71	3q21
8	227129_x_at		-1.69	3.76E-07	9.12E-04	-0.61	-5.70	
9	221492_s_at	APG3	-1.56	5.99E-07	1.20E-03	-0.63	-5.67	3q13.13
10	210048_at	NAPG	-1.46	8.33E-07	1.39E-03	-0.65	-5.67	18p11.21
11	207549_x_at	MCP	-1.33	4.14E-07	9.12E-04	-0.60	-5.66	1q32
12	224851_at		2.00	2.35E-07	9.12E-04	0.56	5.59	
13	218217_at	RISC	-3.65	1.17E-06	1.57E-03	-0.65	-5.59	17q23.1
14	40016_g_at	KIAA0303	1.75	2.06E-07	9.12E-04	0.55	5.58	5q12.3
15	218728_s_at	HSPC163	-2.10	1.16E-06	1.57E-03	-0.65	-5.58	1q42.12

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
16	224759_s_at	MGC17943	1.95	2.48E-07	9.12E-04	0.55	5.54	12q24.11
17	221036_s_at	PSFL	-1.61	1.47E-06	1.57E-03	-0.63	-5.50	15q21.3
18	226353_at	SPPL2A	-1.71	1.36E-06	1.57E-03	-0.62	-5.48	15q15.3
19	200654_at	P4HB	-1.58	6.63E-07	1.25E-03	-0.57	-5.48	17q25
20	209153_s_at	TCF3	1.74	3.72E-07	9.12E-04	0.55	5.47	19p13.3
21	220034_at	IRAK3	-1.74	1.63E-06	1.57E-03	-0.63	-5.47	12q14.1
22	242963_at	MGC26963	-1.85	7.57E-07	1.34E-03	-0.57	-5.45	4q25
23	204165_at	WASF1	2.54	3.84E-07	9.12E-04	0.54	5.44	6q21-q22
24	226276_at	LOC153339	-1.81	2.32E-06	1.89E-03	-0.64	-5.42	5q14.1
25	201360_at	CST3	-2.49	1.60E-06	1.57E-03	-0.60	-5.41	20p11.21
26	227184_at		-3.24	3.44E-06	2.16E-03	-0.67	-5.37	
27	200748_s_at	FTH1	-1.47	1.46E-06	1.57E-03	-0.58	-5.36	11q13
28	217898_at	LOC56851	-1.34	1.39E-06	1.57E-03	-0.57	-5.33	15q13.2
29	223559_s_at	HSPC043	-1.64	2.17E-06	1.87E-03	-0.59	-5.32	9q32
30	223664_x_at	BCL2L13	-1.41	2.73E-06	1.91E-03	-0.59	-5.27	22q11
31	222992_s_at	NDUFB9	-1.39	1.59E-06	1.57E-03	-0.55	-5.27	8q13.3
32	225899_x_at		-1.69	1.91E-06	1.71E-03	-0.56	-5.24	
33	209377_s_at	HMGN3	1.42	1.00E-06	1.57E-03	0.52	5.24	6q14.2
34	205033_s_at	DEFA1	-1.99	1.67E-06	1.57E-03	-0.54	-5.22	8p23.2-p23.1
35	201858_s_at	PRG1	-1.44	1.35E-06	1.57E-03	-0.53	-5.21	10q22.1
36	226240_at	MGC21874	-1.66	2.47E-06	1.91E-03	-0.56	-5.21	4p16.1
37	201412_at	LRP10	-1.49	2.61E-06	1.91E-03	-0.56	-5.21	14q11.2
38	200720_s_at	ACTR1A	-1.44	4.38E-06	2.16E-03	-0.60	-5.18	10q24.32
39	238127_at		2.06	1.21E-06	1.57E-03	0.52	5.18	
40	206861_s_at	CGGBP1	-1.32	3.26E-06	2.13E-03	-0.57	-5.18	3p12-p11.1
41	207275_s_at	FACL1	-2.54	4.40E-06	2.16E-03	-0.59	-5.17	3q13
42	222753_s_at	FLJ22649	-1.57	5.48E-06	2.39E-03	-0.61	-5.16	4q34.2
43	208934_s_at	LGALS8	-1.52	4.67E-06	2.23E-03	-0.59	-5.16	1q42-q43
44	228685_at		-2.04	4.00E-06	2.16E-03	-0.57	-5.15	
45	222586_s_at	OSBPL11	-1.85	5.33E-06	2.37E-03	-0.59	-5.12	3q21
46	219497_s_at	BCL11A	2.25	1.66E-06	1.57E-03	0.51	5.12	2p15
47	223299_at	LOC90701	-1.59	4.28E-06	2.16E-03	-0.57	-5.12	18q21.31
48	217739_s_at	PBEF	-1.89	4.00E-06	2.16E-03	-0.56	-5.12	7q22.1
49	241692_at		-1.80	3.94E-06	2.16E-03	-0.55	-5.10	
50	209744_x_at	ITCH	-1.53	6.83E-06	2.73E-03	-0.60	-5.10	20q11.22-q11.23

6.9 AML M1 versus AML M5a

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	201015_s_at	JUP	8.66	3.01E-12	7.24E-08	0.95	8.32	17q21
2	213258_at		4.67	7.35E-09	2.52E-05	0.91	7.42	
3	225248_at	SPPL2B	2.93	8.59E-10	1.03E-05	0.80	7.04	19p13.3
4	213541_s_at	ERG	3.31	7.17E-09	2.52E-05	0.84	7.03	21q22.3
5	219686_at	HSA250839	6.24	1.40E-09	1.13E-05	0.81	6.99	4p16.2

6	210664_s_at	TFPI	3.90	6.20E-08	1.15E-04	0.84	6.82	2q31-q32.1
7	212071_s_at	SPTBN1	2.27	2.20E-08	6.62E-05	0.82	6.82	2p21
8	210665_at	TFPI	5.48	3.34E-09	2.01E-05	0.76	6.71	2q31-q32.1
9	235142_at	MGC17919	3.30	5.28E-08	1.06E-04	0.81	6.67	1p34.3
10	239247_at		3.65	3.90E-07	3.03E-04	0.85	6.63	
11	225233_at		4.53	6.10E-09	2.52E-05	0.76	6.60	
12	225240_s_at		3.23	5.26E-08	1.06E-04	0.78	6.51	
13	218312_s_at	FLJ12895	2.86	1.39E-06	5.68E-04	0.86	6.47	19q13.43
14	213056_at	KIAA1013	2.27	8.95E-08	1.40E-04	0.78	6.46	3p14.1
15	223162_s_at	LCHN	1.79	5.97E-07	3.88E-04	0.82	6.42	7q34
16	214966_at	GRIK5	3.27	1.23E-07	1.41E-04	0.78	6.40	19q13.2
17	235052_at	FLJ38451	3.45	4.38E-07	3.18E-04	0.78	6.27	19q13.11
18	226550_at		2.51	6.78E-08	1.16E-04	0.73	6.25	
19	208056_s_at	CBFA2T3	2.20	1.11E-07	1.40E-04	0.74	6.23	16q24
20	205239_at	AREG	4.68	2.74E-08	7.32E-05	0.71	6.21	4q13-q21
21	227564_at	FLJ32731	2.97	3.26E-08	7.85E-05	0.70	6.17	8p11.1
22	203069_at	SV2A	3.53	1.09E-07	1.40E-04	0.70	6.03	1q21.2
23	231561_s_at	APOC2	-1.92	3.41E-05	6.28E-03	-0.97	-6.01	19q13.2
24	235199_at		2.24	2.78E-06	9.15E-04	0.78	-5.99	
25	220981_x_at	NXF2	-1.83	6.22E-06	1.66E-03	-0.81	-5.96	Xq22-q23
26	230894_s_at		4.19	1.96E-06	7.13E-04	0.76	5.94	
27	204529_s_at	TOX	3.25	9.92E-08	1.40E-04	0.68	5.93	8q11.23
28	209676_at	TFPI	2.40	5.93E-06	1.62E-03	0.80	5.92	2q31-q32.1
29	238732_at	COL24A1	4.68	9.42E-08	1.40E-04	0.68	5.92	1p22.2
30	242051_at		3.07	2.10E-07	2.02E-04	0.69	5.91	
31	232438_at	EPS15R	2.75	1.20E-07	1.41E-04	0.67	5.85	19p13.11
32	225611_at	KIAA0303	2.18	3.36E-07	2.70E-04	0.69	5.84	5q12.3
33	209160_at	AKR1C3	3.65	4.06E-06	1.24E-03	0.76	5.83	10p15-p14
34	230158_at	FLJ32949	4.00	1.71E-07	1.79E-04	0.67	5.82	12q14.1
35	232618_at	CYorf15A	5.89	1.42E-07	1.56E-04	0.66	5.81	Y
36	204352_at	TRAF5	3.13	1.22E-06	5.64E-04	0.71	5.80	1q32
37	227576_at		3.56	2.54E-07	2.26E-04	0.67	5.79	
38	212618_at	KIAA0295	3.19	1.87E-07	1.88E-04	0.66	5.77	15q22.1
39	208826_x_at	HINT1	1.49	6.17E-06	1.66E-03	0.76	5.76	5q31.2
40	217936_at		2.26	2.43E-07	2.25E-04	0.66	5.75	
41	204639_at	ADA	2.79	1.31E-06	5.68E-04	0.70	5.74	20q12-q13.11
42	239251_at		2.37	4.39E-07	3.18E-04	0.67	5.73	
43	236198_at		3.45	2.72E-07	2.34E-04	0.65	5.67	
44	229530_at		4.20	2.82E-07	2.34E-04	0.64	5.65	
45	212385_at		2.99	1.38E-06	5.68E-04	0.67	5.61	
46	207735_at	FLJ20456	2.21	1.57E-06	5.98E-04	0.68	5.61	18q12.1
47	206265_s_at	GPLD1	-2.95	9.74E-05	1.25E-02	-0.95	-5.58	6p22.3-p22.2
48	225238_at		3.29	5.56E-07	3.71E-04	0.64	5.57	
49	224576_at	KIAA1181	1.89	2.74E-06	9.15E-04	0.68	5.56	5q35.2
50	207721_x_at	HINT1	1.60	1.50E-05	3.27E-03	0.75	5.56	5q31.2

6.10	AML M1 versus AML M5b							
#	affy Id	HUGO name	fc	p	q	stn	t	Map Location
1	221731_x_at	CSPG2	-6.69	3.67E-11	1.79E-08	-1.67	-11.80	5q14.3
2	204620_s_at	CSPG2	-6.58	9.75E-11	3.58E-08	-1.73	-11.75	5q14.3
3	202803_s_at	ITGB2	-2.54	1.77E-12	2.89E-09	-1.45	-11.36	21q22.3
4	200871_s_at	PSAP	-2.69	8.41E-12	6.26E-09	-1.44	-11.08	10q21-q22
5	204158_s_at	TCIRG1	-2.59	3.02E-11	1.56E-08	-1.45	-10.91	11q13.4-q13.5
6	228402_at	MGC15435	2.87	2.41E-17	3.50E-13	1.20	10.87	5q13.2
7	201360_at	CST3	-3.74	3.81E-11	1.82E-08	-1.44	-10.79	20p11.21
8	200953_s_at	CCND2	3.71	2.61E-17	3.50E-13	1.18	10.78	12p13
9	218217_at	RISC	-6.92	1.01E-09	2.27E-07	-1.66	-10.77	17q23.1
10	212501_at	CEBPB	-2.55	2.48E-11	1.38E-08	-1.38	-10.58	20q13.1
11	204971_at	CSTA	-3.37	1.29E-11	8.07E-09	-1.34	-10.51	3q21
12	205786_s_at	ITGAM	-3.33	2.91E-10	8.58E-08	-1.41	-10.25	16p11.2
13	216041_x_at	GRN	-3.98	2.81E-10	8.37E-08	-1.40	-10.22	17q21.32
14	202363_at	SPOCK	-2.73	9.05E-11	3.47E-08	-1.33	-10.12	5q31
15	200678_x_at	GRN	-3.71	3.92E-10	1.08E-07	-1.38	-10.05	17q21.32
16	210664_s_at	TFPI	5.62	1.31E-15	1.17E-11	1.11	10.02	2q31-q32.1
17	203973_s_at	CEBPD	-3.18	1.95E-11	1.14E-08	-1.24	-9.95	8p11.2-p11.1
18	35820_at	GM2A	-2.89	1.83E-09	3.53E-07	-1.44	-9.89	5q31.3-q33.1
19	208361_s_at	BN51T	3.41	8.73E-15	3.90E-11	1.10	9.83	8q21
20	235109_at		7.99	2.60E-15	1.74E-11	1.07	9.76	
21	235142_at	MGC17919	5.43	5.46E-15	2.93E-11	1.05	9.60	1p34.3
22	217728_at	S100A6	-3.46	1.21E-09	2.65E-07	-1.32	-9.57	1q21
23	228648_at	LRG	-3.49	9.03E-10	2.12E-07	-1.29	-9.51	19p13.3
24	221841_s_at		-3.09	1.34E-10	4.59E-08	-1.21	-9.50	
25	209676_at	TFPI	2.94	2.03E-14	7.74E-11	1.05	9.49	2q31-q32.1
26	213622_at	COL9A2	-2.36	2.96E-09	5.11E-07	-1.32	-9.33	1p33-p32
27	206267_s_at	MATK	3.17	1.08E-11	7.25E-09	1.11	9.32	19p13.3
28	200886_s_at	PGAM1	-2.10	1.12E-09	2.46E-07	-1.25	-9.31	10q25.3
29	211284_s_at	GRN	-4.09	2.62E-09	4.68E-07	-1.30	-9.31	17q21.32
30	213258_at		4.68	2.31E-14	7.74E-11	1.02	9.28	
31	205180_s_at	ADAM8	-2.79	5.01E-10	1.30E-07	-1.19	-9.16	10q26.3
32	203520_s_at	ZFP318	-3.07	1.48E-08	1.84E-06	-1.39	-9.10	6pter-p12.1
33	215075_s_at	GRB2	-1.99	6.59E-09	9.70E-07	-1.30	-9.08	17q24-q25
34	231982_at		9.27	8.63E-14	2.57E-10	0.99	9.00	
35	201963_at	FACL2	-2.94	1.41E-08	1.80E-06	-1.34	-8.97	4q34-q35
36	217988_at	HEI10	2.16	2.55E-12	3.30E-09	1.03	8.96	14q11.1
37	224851_at		3.42	3.07E-13	6.86E-10	1.00	8.96	
38	224826_at	KIAA1434	-2.38	8.73E-10	2.09E-07	-1.15	-8.89	20p12.3
39	214298_x_at	SEPT6	2.57	1.53E-13	4.11E-10	0.98	8.89	Xq24

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
40	229101_at		-3.33	9.79E-09	1.33E-06	-1.28	-8.88	
41	202388_at	RGS2	-2.07	3.98E-11	1.87E-08	-1.05	-8.83	1q31
42	212807_s_at	SORT1	-4.17	5.19E-08	4.54E-06	-1.46	-8.82	1p21.3-p13.1
43	218086_at	NPDC1	12.03	8.05E-13	1.44E-09	1.03	8.82	9q34.3
44	244741_s_at		4.04	1.88E-13	4.57E-10	0.97	8.81	
45	208438_s_at	FGR	-4.84	3.00E-08	2.99E-06	-1.35	-8.77	1p36.2-p36.1
46	235670_at		-3.99	1.37E-08	1.77E-06	-1.27	-8.77	
47	204165_at	WASF1	5.17	5.32E-13	1.10E-09	0.95	8.60	6q21-q22
48	203140_at	BCL6	-3.46	2.32E-08	2.53E-06	-1.26	-8.59	3q27
49	222496_s_at	FLJ20273	-5.14	3.34E-08	3.22E-06	-1.29	-8.57	4p13-p12
50	211742_s_at	EVI2B	-2.47	7.97E-09	1.11E-06	-1.17	-8.57	17q11.2

6.11 AML M1 versus AML M6

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211070_x_at	DBI	3.18	2.90E-19	2.98E-15	1.49	12.78	2q12-q21
2	235463_s_at	LOC253782	2.43	2.03E-19	2.98E-15	1.47	12.63	2q31.1
3	228209_at		5.50	9.08E-18	4.67E-14	1.48	12.54	
4	202428_x_at	DBI	2.92	3.27E-18	2.24E-14	1.44	12.29	2q12-q21
5	225605_at	LOC90313	5.84	1.32E-17	5.17E-14	1.34	11.57	17q11.1
6	235056_at		3.07	1.51E-17	5.17E-14	1.32	11.38	
7	224916_at		3.54	5.13E-16	1.51E-12	1.20	10.38	
8	202262_x_at	DDAH2	2.44	1.99E-12	2.40E-09	1.27	10.33	6p21.3
9	206674_at	FLT3	5.66	4.62E-14	8.64E-11	1.22	10.26	13q12
10	221666_s_at	ASC	4.69	1.05E-14	2.40E-11	1.19	10.14	16p12-p11.2
11	206081_at	SLC24A1	4.98	4.23E-15	1.09E-11	1.15	9.95	15q22
12	214909_s_at	DDAH2	3.27	4.32E-13	6.83E-10	1.19	9.92	6p21.3
13	201029_s_at	CD99	2.10	5.73E-12	4.26E-09	1.15	9.46	Xp22.32
14	201037_at	PFKP	3.59	2.90E-14	5.97E-11	1.09	9.43	10p15.3-p15.2
15	223364_s_at	DDX37	4.49	6.00E-12	4.26E-09	1.14	9.42	12q24.31
16	212442_s_at	LOC253782	2.80	1.21E-12	1.66E-09	1.10	9.29	2q31.1
17	222640_at	DNMT3A	2.34	8.04E-13	1.18E-09	1.09	9.24	2p23
18	209389_x_at	DBI	2.44	5.17E-12	4.26E-09	1.11	9.24	2q12-q21
19	203096_s_at	PDZ-GEF1	-2.30	9.71E-07	4.91E-05	-1.50	-9.23	4q32.1
20	224851_at		3.78	8.98E-12	5.59E-09	1.11	9.21	
21	224929_at		2.93	1.11E-13	1.91E-10	1.05	9.13	
22	218218_at	DIP13B	-1.48	3.30E-11	1.34E-08	-1.10	-9.03	12q24.1
23	215537_x_at	DDAH2	2.49	1.65E-11	7.87E-09	1.08	8.98	6p21.3
24	201561_s_at	CLSTN1	2.44	1.50E-10	4.40E-08	1.11	8.95	1p36.22
25	210829_s_at	SSBP2	3.04	1.97E-11	9.03E-09	1.08	8.92	5q14.1
26	202659_at	PSMB10	2.82	1.35E-11	6.95E-09	1.07	8.91	16q22.1
27	228242_at		2.86	3.07E-12	3.10E-09	1.05	8.89	
28	209539_at	ARHGEF6	2.22	1.44E-12	1.85E-09	1.04	8.85	Xq26

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
29	217286_s_at	NDRG3	3.11	4.31E-12	3.85E-09	1.05	8.85	20q11.21-q11.23
30	210624_s_at	ILVBL	1.74	6.80E-10	1.65E-07	1.11	8.80	19p13.1
31	201613_s_at	RUVBL1	2.92	3.29E-11	1.34E-08	1.06	8.79	3q21
32	225045_at	FLJ10392	4.37	3.97E-10	1.03E-07	1.08	8.72	2p16.1
33	224649_x_at	CFP1	2.44	3.41E-12	3.19E-09	1.02	8.68	10p11.21
34	221710_x_at	FLJ10647	3.70	2.73E-11	1.17E-08	1.04	8.67	1p34.3
35	223015_at	eIF2a	1.46	5.17E-10	1.30E-07	1.08	8.66	3q25.1
36	225473_at	LOC149670	3.74	2.94E-09	5.51E-07	1.11	8.63	20q11.22
37	223647_x_at	HSC20	1.92	8.18E-11	2.78E-08	1.05	8.62	22q12.1
38	239068_at	LOC285831	-1.61	2.22E-08	2.55E-06	-1.15	-8.60	6p21.31
39	222825_at	CGI-77	2.34	1.69E-10	4.88E-08	1.05	8.60	8q21.3
40	225421_at	LOC135293	3.65	3.17E-12	3.10E-09	1.00	8.58	6q16.1
41	200036_s_at - HG-U133B	RPL10A	1.16	3.09E-12	3.10E-09	1.00	8.57	6p21.3-p21.2
42	225029_at		2.14	1.31E-11	6.93E-09	1.01	8.56	
43	201536_at	DUSP3	2.58	5.87E-11	2.16E-08	1.03	8.56	17q21
44	207711_at		3.40	1.22E-09	2.66E-07	1.07	8.53	
45	201061_s_at	STOM	-2.58	7.77E-06	2.39E-04	-1.57	-8.49	9q34.1
46	226116_at		2.02	1.44E-11	7.22E-09	1.00	8.49	
47	226521_s_at	FLJ13614	2.07	5.71E-12	4.26E-09	0.99	8.48	4q21.21-q21.23
48	204639_at	ADA	3.88	2.26E-12	2.59E-09	0.98	8.45	20q12-q13.11
49	1294_at	UBE1L	2.28	5.71E-12	4.26E-09	0.98	8.44	3p21
50	227156_at		4.23	1.15E-11	6.23E-09	0.99	8.41	

6.12 AML M2 versus AML M4

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	202576_s_at	FLJ11126	-1.39	2.70E-06	7.81E-02	-0.52	-5.07	16q22.1
2	201360_at	CST3	-2.23	6.86E-06	7.81E-02	-0.56	-5.01	20p11.21
3	202113_s_at	SNX2	-1.61	8.38E-06	7.81E-02	-0.55	-4.94	5q23
4	221492_s_at	APG3	-1.43	1.41E-05	9.18E-02	-0.54	-4.81	3q13.13
5	223950_s_at	DKFZp761A132	-1.44	7.85E-06	7.81E-02	-0.48	-4.76	16p13.3
6	224983_at		-1.56	1.76E-05	9.18E-02	-0.53	-4.74	
7	226276_at	LOC153339	-1.65	2.54E-05	9.18E-02	-0.54	-4.66	5q14.1
8	222586_s_at	OSBPL11	-1.69	3.27E-05	9.18E-02	-0.54	-4.61	3q21
9	202941_at	NDUFV2	-1.32	2.91E-05	9.18E-02	-0.48	-4.52	18p11.31-p11.2
10	224717_s_at	MGC2747	-1.31	3.02E-05	9.18E-02	-0.48	-4.51	19p13.11
11	208890_s_at	PLXNB2	-1.69	3.78E-05	9.18E-02	-0.50	-4.50	22q13.33
12	224465_s_at	PYM	-1.58	3.52E-05	9.18E-02	-0.48	-4.48	12q13.13
13	227413_at	MGC10067	-1.45	4.27E-05	9.36E-02	-0.48	-4.43	5q33.3
14	207530_s_at	CDKN2B	2.07	3.32E-05	9.18E-02	0.44	4.38	9p21
15	205311_at	DDC	2.09	2.98E-05	9.18E-02	0.43	4.37	7p11
16	210549_s_at	CCL23	-3.52	7.88E-05	9.88E-02	-0.53	-4.37	17q12

#	affy Id	HUGO name	fc	p	q	stn	t	Map Location
17	221078_s_at	FLJ10392	-1.33	3.94E-05	9.18E-02	-0.44	-4.36	2p16.1
18	210443_x_at	OGFR	-1.51	6.66E-05	9.88E-02	-0.49	-4.35	20q13.3
19	215532_x_at	KIAA1473	1.70	3.53E-05	9.18E-02	0.43	4.33	19p11
20	202841_x_at	OGFR	-1.57	6.90E-05	9.88E-02	-0.48	-4.33	20q13.3
21	243806_at		-1.56	5.74E-05	9.88E-02	-0.46	-4.32	
22	225593_at	LSM10	-1.49	7.84E-05	9.88E-02	-0.48	-4.30	1p34.3
23	34689_at	TREX1	-1.42	6.08E-05	9.88E-02	-0.45	-4.29	3p21.3-p21.2
24	209189_at	FOS	-1.79	6.98E-05	9.88E-02	-0.46	-4.29	14q24.3
25	221841_s_at		-1.79	6.83E-05	9.88E-02	-0.45	-4.26	
26	201157_s_at	NMT1	-1.50	7.73E-05	9.88E-02	-0.46	-4.26	17q21.31
27	226807_at	FLJ34243	1.50	5.21E-05	9.88E-02	0.42	4.25	16q22.3
28	224374_s_at	EMILIN-2	-1.65	9.55E-05	1.03E-01	-0.48	-4.25	18p11.3
29	216015_s_at	CIAS1	-2.00	1.15E-04	1.12E-01	-0.50	-4.23	1q44
30	201646_at		-1.33	6.80E-05	9.88E-02	-0.43	-4.22	
31	212910_at	HRIHFB2206	-1.45	9.96E-05	1.03E-01	-0.47	-4.21	16q22.1
32	220266_s_at	KLF4	-3.08	1.40E-04	1.13E-01	-0.52	-4.20	9q31
33	226818_at	LOC219972	-3.01	1.51E-04	1.13E-01	-0.53	-4.18	11q12.1
34	209616_s_at	CES1	-5.99	1.65E-04	1.13E-01	-0.56	-4.18	16q13-q22.1
35	222503_s_at	FLJ10904	-1.34	9.65E-05	1.03E-01	-0.45	-4.17	5q13.2
36	204619_s_at	CSPG2	-3.57	1.62E-04	1.13E-01	-0.53	-4.17	5q14.3
37	238451_at	FLJ32798	-2.27	1.66E-04	1.13E-01	-0.52	-4.15	10p11.1
38	221036_s_at	PSFL	-1.41	1.35E-04	1.13E-01	-0.47	-4.14	15q21.3
39	222842_at	AGO4	-1.60	1.17E-04	1.12E-01	-0.45	-4.13	1p34.3
40	206240_s_at	ZNF136	1.35	8.43E-05	9.88E-02	0.41	4.13	19p13.2-p13.12
41	47560_at	FLJ11939	1.73	7.86E-05	9.88E-02	0.41	4.12	19p13.12
42	230896_at		3.39	8.19E-05	9.88E-02	0.41	4.12	
43	228707_at	LOC137075	-2.22	1.38E-04	1.13E-01	-0.46	-4.11	8p23.1
44	213549_at	PRO2730	1.58	8.49E-05	9.88E-02	0.41	4.11	3p21.31
45	213187_x_at		-1.22	1.09E-04	1.09E-01	-0.42	-4.09	
46	222581_at	XPR1	-1.61	1.48E-04	1.13E-01	-0.45	-4.08	1q25.1
47	221561_at	SOAT1	-1.70	1.47E-04	1.13E-01	-0.44	-4.07	1q25
48	223598_at	RAD23B	1.45	9.62E-05	1.03E-01	0.40	4.06	9q31.2
49	205859_at	LY86	-2.22	1.83E-04	1.13E-01	-0.47	-4.06	6p24.3
50	212820_at	RC3	-1.72	1.66E-04	1.13E-01	-0.45	-4.06	15q15.3

6.13 AML M2 versus AML M5a

#	affy Id	HUGO name	fc	p	q	stn	t	Map Location
1	210665_at	TFPI	5.48	2.02E-09	7.03E-05	0.77	6.81	2q31-q32.1
2	242028_at	FLJ38281	2.22	5.96E-09	7.03E-05	0.77	6.73	19p13.13
3	201015_s_at	JUP	8.13	4.74E-09	7.03E-05	0.75	6.63	17q21
4	223714_at	ZNF256	2.70	7.09E-08	2.82E-04	0.79	6.58	19q13.43
5	200602_at	APP	6.28	1.23E-08	1.08E-04	0.72	6.39	21q21.3

6	227839_at	MBD5	4.43	2.81E-08	1.99E-04	0.71	6.22	2q23.2
7	212071_s_at	SPTBN1	2.41	4.68E-08	2.36E-04	0.71	6.21	2p21
8	213541_s_at	ERG	2.64	1.65E-06	2.38E-03	0.80	6.18	21q22.3
9	214953_s_at	APP	3.73	3.84E-08	2.26E-04	0.70	6.14	21q21.3
10	226342_at		4.68	7.17E-08	2.82E-04	0.69	6.06	
11	219266_at	ZBRK1	2.17	4.39E-07	1.03E-03	0.73	6.04	19q13.41
12	231561_s_at	APOC2	-1.97	2.13E-05	1.16E-02	-0.91	-6.02	19q13.2
13	218778_x_at	EPS8R1	2.43	8.58E-08	3.03E-04	0.68	5.98	19q13.42
14	230805_at		3.65	1.15E-07	3.39E-04	0.67	5.89	
15	205239_at	AREG	4.61	1.10E-07	3.39E-04	0.66	5.86	4q13-q21
16	241769_at		4.51	1.97E-07	5.35E-04	0.67	5.77	
17	214966_at	GRIK5	3.19	7.13E-07	1.48E-03	0.67	5.67	19q13.2
18	210664_s_at	TFPI	3.77	8.05E-07	1.58E-03	0.66	5.62	2q31-q32.1
19	219686_at	HSA250839	4.49	3.72E-07	9.38E-04	0.64	5.60	4p16.2
20	203429_s_at	C1orf9	1.88	4.18E-06	4.76E-03	0.69	5.53	1q24
21	203544_s_at	STAM	1.98	2.94E-06	3.80E-03	0.67	5.51	10p14-p13
22	225248_at	SPPL2B	2.22	6.84E-07	1.48E-03	0.63	5.51	19p13.3
23	206240_s_at	ZNF136	1.55	7.64E-06	6.14E-03	0.70	5.47	19p13.2-p13.12
24	212558_at	SPRY1	2.99	1.69E-06	2.38E-03	0.62	5.36	4q27
25	212249_at	PIK3R1	2.30	9.12E-07	1.70E-03	0.61	5.35	5q12-q13
26	203783_x_at	POLRMT	3.03	1.29E-06	2.18E-03	0.61	5.34	19p13.3
27	223000_s_at	F11R	2.07	3.33E-05	1.52E-02	0.73	5.33	1q21.2-q21.3
28	217951_s_at	PHF3	1.66	8.40E-06	6.32E-03	0.66	5.30	
29	230541_at	LOC149134	3.05	1.20E-06	2.12E-03	0.60	5.28	1q44
30	209099_x_at	JAG1	2.76	1.37E-06	2.20E-03	0.60	5.27	20p12.1-p11.23
31	232438_at	EPS15R	2.29	1.57E-06	2.38E-03	0.59	5.22	19p13.11
32	237470_at		2.49	1.04E-05	7.38E-03	0.64	5.18	
33	235052_at	FLJ38451	3.15	7.45E-06	6.12E-03	0.62	5.14	19q13.11
34	215359_x_at	ZNF44	1.53	6.77E-06	5.98E-03	0.61	5.10	16p11
35	228366_at	SID6-306	1.61	2.62E-06	3.57E-03	0.58	5.08	4q25
36	226442_at	ABTB1	4.63	3.01E-06	3.80E-03	0.59	5.08	3q21
37	201829_at	NET1	1.99	5.98E-06	5.71E-03	0.60	5.06	10p15
38	207244_x_at	CYP2A6	2.86	3.23E-06	3.81E-03	0.57	5.05	19q13.2
39	217936_at		1.95	5.36E-06	5.52E-03	0.59	5.04	
40	244779_at		2.19	3.74E-05	1.67E-02	0.66	5.04	
41	223708_at	C1QTNF4	7.13	3.20E-06	3.81E-03	0.57	5.03	11q11
42	214230_at	CDC42	1.90	5.47E-06	5.52E-03	0.58	5.01	1p36.1
43	206009_at	ITGA9	2.43	2.73E-05	1.35E-02	0.63	4.99	3p21.3
44	215918_s_at	SPTBN1	2.48	5.10E-06	5.46E-03	0.57	4.98	2p21
45	239251_at		1.93	2.62E-05	1.32E-02	0.62	4.96	
46	209332_s_at	MAX	1.46	2.42E-05	1.24E-02	0.62	4.96	14q23
47	214043_at		3.29	4.35E-06	4.80E-03	0.56	4.95	
48	204449_at	PDCL	1.77	6.65E-06	5.98E-03	0.57	4.94	9q12-q13
49	219711_at	FLJ20070	1.69	2.75E-05	1.35E-02	0.61	4.90	19q13.43
50	207530_s_at	CDKN2B	2.39	5.90E-06	5.71E-03	0.55	4.88	9p21

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
	6.14	AML M2 versus AML M5b						
1	221731_x_at	CSPG2	-5.77	1.08E-10	2.34E-07	-1.71	-11.69	5q14.3
2	204620_s_at	CSPG2	-5.45	2.28E-10	3.09E-07	-1.69	-11.38	5q14.3
3	35820_at	GM2A	-3.17	9.68E-10	7.66E-07	-1.54	-10.41	5q31.3-q33.1
4	201360_at	CST3	-3.35	1.09E-10	2.34E-07	-1.39	-10.39	20p11.21
5	203973_s_at	CEBPD	-2.66	3.51E-10	4.00E-07	-1.26	-9.57	8p11.2-p11.1
6	221841_s_at		-2.89	4.02E-10	4.41E-07	-1.23	-9.43	
7	202803_s_at	ITGB2	-1.98	2.47E-10	3.20E-07	-1.21	-9.39	21q22.3
8	202363_at	SPOCK	-2.42	4.42E-10	4.53E-07	-1.21	-9.32	5q31
9	218217_at	RISC	-3.96	7.37E-09	3.35E-06	-1.37	-9.27	17q23.1
10	210427_x_at	ANXA2	-2.64	2.78E-09	1.49E-06	-1.27	-9.20	15q21-q22
11	201590_x_at	ANXA2	-2.64	3.45E-09	1.79E-06	-1.28	-9.17	15q21-q22
12	204158_s_at	TCIRG1	-2.24	1.16E-10	2.34E-07	-1.13	-9.14	11q13.4-q13.5
13	243364_at	AUTS2	5.55	5.06E-14	1.44E-09	0.99	9.08	7q11.21
14	213503_x_at	ANXA2	-2.68	6.61E-09	3.14E-06	-1.25	-8.90	15q21-q22
15	216041_x_at	GRN	-2.71	1.04E-08	4.16E-06	-1.26	-8.84	17q21.32
16	200678_x_at	GRN	-2.64	1.33E-08	4.91E-06	-1.28	-8.83	17q21.32
17	200953_s_at	CCND2	3.39	2.41E-13	3.44E-09	0.96	8.76	12p13
18	200871_s_at	PSAP	-2.00	1.14E-09	8.11E-07	-1.10	-8.65	10q21-q22
19	204971_at	CSTA	-2.33	1.53E-09	9.89E-07	-1.09	-8.54	3q21
20	212737_at	GM2A	-2.67	5.02E-08	1.14E-05	-1.31	-8.52	5q31.3-q33.1
21	229860_x_at		-2.14	2.24E-08	6.73E-06	-1.21	-8.47	
22	238417_at	FLJ32029	1.82	3.40E-12	3.23E-08	0.90	8.24	11q13.3
23	217728_at	S100A6	-2.63	1.32E-08	4.91E-06	-1.10	-8.20	1q21
24	210549_s_at	CCL23	-7.67	2.20E-07	3.15E-05	-1.40	-8.15	17q12
25	211284_s_at	GRN	-2.81	5.52E-08	1.20E-05	-1.17	-8.09	17q21.32
26	211612_s_at	IL13RA1	-2.45	5.07E-08	1.15E-05	-1.15	-8.05	Xq24
27	212463_at		3.08	5.69E-12	4.05E-08	0.88	8.05	
28	204169_at	IMPDH1	-1.93	3.25E-08	8.51E-06	-1.11	-8.02	7q31.3-q32
29	203588_s_at	TFDP2	2.44	5.08E-11	1.61E-07	0.90	8.01	3q23
30	200985_s_at	CD59	3.57	7.86E-12	4.48E-08	0.87	7.99	11p13
31	231982_at		7.27	1.51E-11	6.16E-08	0.88	7.97	
32	226276_at	LOC153339	-2.43	1.68E-07	2.59E-05	-1.24	-7.95	5q14.1
33	202877_s_at	C1QR1	-3.03	1.45E-07	2.34E-05	-1.22	-7.94	20p11.21
34	200839_s_at	CTSB	-2.57	8.57E-08	1.65E-05	-1.16	-7.93	8p22
35	235779_at		2.73	2.02E-10	3.03E-07	0.91	7.89	
36	233849_s_at	ARHGAP5	4.18	1.27E-11	6.04E-08	0.86	7.88	14q12
37	203769_s_at	STS	-3.04	2.72E-07	3.56E-05	-1.29	-7.87	Xp22.32
38	210524_x_at	MT1F	-2.38	1.25E-07	2.11E-05	-1.17	-7.86	16q13
39	205859_at	LY86	-4.09	2.28E-07	3.18E-05	-1.24	-7.84	6p24.3

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
40	203186_s_at	S100A4 -	-2.35	4.28E-08	1.03E-05	-1.05	-7.75	1q21
41	235678_at		-2.86	4.16E-07	4.84E-05	-1.30	-7.72	
42	200886_s_at	PGAM1	-1.73	7.61E-08	1.52E-05	-1.07	-7.69	10q25.3
43	201944_at	HEXB	-2.69	3.47E-07	4.29E-05	-1.23	-7.67	5q13
44	212807_s_at	SORT1	-2.91	4.74E-07	5.35E-05	-1.29	-7.66	1p21.3-p13.1
45	204057_at	ICSBP1	-2.66	1.32E-08	4.91E-06	-0.96	-7.60	16q24.1
46	228974_at		3.05	4.42E-11	1.58E-07	0.83	7.59	
47	201127_s_at	ACLY	-1.63	1.86E-08	5.84E-06	-0.96	-7.57	17q12-q21
48	210664_s_at	TFPI	5.43	8.28E-11	2.34E-07	0.84	7.57	2q31-q32.1
49	212501_at	CEBPB	-1.86	7.65E-09	3.35E-06	-0.92	-7.51	20q13.1
50	219505_at	CECR1	-3.87	5.60E-07	5.98E-05	-1.24	-7.51	22q11.2

6.15 AML M2 versus AML M6

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211070_x_at	DBI	2.62	6.40E-15	1.80E-10	1.23	10.52	2q12-q21
2	202428_x_at	DBI	2.45	2.47E-14	2.31E-10	1.22	10.36	2q12-q21
3	221928_at	LOC283445	4.42	2.07E-14	2.31E-10	1.11	9.60	12q24.12
4	213870_at	COL11A2	3.68	4.67E-13	3.28E-09	1.03	8.95	6p21.3
5	235463_s_at	LOC253782	2.08	1.36E-12	7.63E-09	0.98	8.57	2q31.1
6	224747_at	LOC92912	1.88	7.84E-12	2.45E-08	0.99	8.51	15q23
7	201105_at	LGALS1	9.06	2.58E-12	1.21E-08	0.99	8.49	22q13.1
8	224916_at		2.80	3.31E-12	1.33E-08	0.96	8.34	
9	225605_at	LOC90313	4.42	6.21E-12	2.18E-08	0.96	8.34	17q11.1
10	228209_at		4.07	2.00E-11	5.61E-08	0.97	8.29	
11	214909_s_at	DDAH2	3.38	2.63E-11	6.15E-08	0.92	7.96	6p21.3
12	221666_s_at	ASC	3.38	5.05E-10	7.47E-07	0.96	7.96	16p12-p11.2
13	202262_x_at	DDAH2	2.52	3.74E-11	8.09E-08	0.92	7.93	6p21.3
14	201850_at	CAPG	3.38	2.23E-11	5.69E-08	0.91	7.88	2cen-q24
15	237209_s_at	NFRKB	3.37	7.52E-09	5.03E-06	0.99	7.87	11q24-q25
16	209389_x_at	DBI	2.11	2.76E-09	2.42E-06	0.97	7.86	2q12-q21
17	217226_s_at	BA108L7.2	2.47	6.26E-11	1.25E-07	0.91	7.84	10q24.31
18	235056_at		2.19	1.10E-10	1.94E-07	0.90	7.76	
19	228415_at	AP1S2	2.18	6.78E-11	1.27E-07	0.89	7.71	Xp22.31
20	220974_x_at	BA108L7.2	3.69	1.54E-10	2.54E-07	0.89	7.63	10q24.31
21	208659_at	CLIC1	1.59	2.17E-07	6.21E-05	1.02	7.61	6p22.1-p21.2
22	225796_at		1.92	4.83E-10	7.47E-07	0.87	7.46	
23	209539_at	ARHGEF6	1.93	8.53E-10	1.04E-06	0.87	7.41	Xq26
24	224649_x_at	CFP1	2.22	6.19E-10	8.69E-07	0.86	7.34	10p11.21
25	224744_at		1.81	1.07E-09	1.25E-06	0.86	7.32	
26	219186_at	DKFZp547O146	-1.65	4.84E-08	1.98E-05	-0.91	-7.24	19p13.3
27	228242_at		2.28	1.02E-08	6.10E-06	0.88	7.22	
28	205081_at	CRIP1	5.94	6.67E-10	8.92E-07	0.83	7.18	7q11.23

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
29	220126_at	TSP50	4.17	7.48E-10	9.55E-07	0.83	7.18	3p14-p12
30	205603_s_at	DIAPH2	2.08	4.27E-07	9.60E-05	0.95	7.17	Xq22
31	221710_x_at	FLJ10647	3.48	1.71E-09	1.85E-06	0.84	7.17	1p34.3
32	223015_at	eIF2a	1.40	1.67E-08	8.69E-06	0.87	7.15	3q25.1
33	200641_s_at	YWHAZ	1.66	5.58E-09	4.02E-06	0.85	7.13	8q23.1
34	58780_s_at	FLJ10357	2.93	2.06E-09	2.06E-06	0.83	7.12	14q11.1
35	213160_at	DOCK2	2.10	3.43E-07	8.18E-05	0.93	7.08	5q35.1
36	229841_at		-1.60	3.66E-07	8.55E-05	-0.93	-7.05	
37	217286_s_at	NDRG3	2.46	1.54E-08	8.31E-06	0.85	7.05	20q11.21-q11.23
38	209876_at	GIT2	2.59	1.37E-07	4.52E-05	0.89	7.03	12q24.1
39	201037_at	PFKP	2.30	2.57E-09	2.35E-06	0.82	7.01	10p15.3-p15.2
40	203927_at	NFKBIE	1.89	1.52E-09	1.71E-06	0.81	7.00	6p21.1
41	203653_s_at	COIL	2.60	3.32E-07	8.04E-05	0.90	6.96	17q22-q23
42	222792_s_at	HSPC128	1.48	2.02E-09	2.06E-06	0.80	6.94	12q21.31
43	223251_s_at	ANKRD10	2.18	4.43E-07	9.86E-05	0.91	6.92	13q33.3
44	210251_s_at	RIPX	2.57	1.34E-08	7.53E-06	0.83	6.92	4q13.3
45	216015_s_at	CIAS1	3.50	2.28E-08	1.12E-05	0.84	6.92	1q44
46	32259_at	EZH1	-1.91	2.71E-05	1.64E-03	-1.17	-6.90	17q21.1-q21.3
47	226608_at	SAS10	1.75	1.07E-08	6.27E-06	0.82	6.89	4q13.3
48	210624_s_at	ILVBL	1.54	3.44E-07	8.18E-05	0.89	6.86	19p13.1
49	228595_at	HSD17B1	3.16	4.14E-09	3.16E-06	0.80	6.85	17q11-q21
50	201561_s_at	CLSTN1	1.97	5.41E-07	1.12E-04	0.90	6.85	1p36.22
6.16	AML M4 versus AML M5a							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205408_at	MLLT10	1.47	3.53E-05	2.30E-01	0.70	4.72	10p12
2	212420_at	ELF1	2.09	5.06E-05	2.30E-01	0.71	4.69	13q13
3	233070_at		3.20	5.64E-05	2.30E-01	0.71	4.66	
4	218778_x_at	EPS8R1	2.57	3.51E-05	2.30E-01	0.68	4.63	19q13.42
5	239067_s_at	PANX2	3.78	3.78E-05	2.30E-01	0.68	4.60	22q13.33
6	210379_s_at	TLK1	2.13	1.35E-04	2.66E-01	0.72	4.56	2q31.1
7	241769_at		3.66	5.95E-05	2.30E-01	0.69	4.52	
8	209599_s_at	HTCD37	2.35	4.93E-05	2.30E-01	0.66	4.52	1q21
9	225576_at	LOC116254	1.62	5.69E-05	2.30E-01	0.66	4.50	6q24.3
10	225248_at	SPPL2B	2.65	5.71E-05	2.30E-01	0.66	4.48	19p13.3
11	204449_at	PDCL	1.60	7.41E-05	2.31E-01	0.66	4.46	9q12-q13
12	236953_s_at	LOC283506	2.45	7.13E-05	2.31E-01	0.65	4.42	13q13.2
13	230805_at		2.91	6.16E-05	2.30E-01	0.64	4.42	
14	210788_s_at	retSDR4	1.45	2.36E-04	2.80E-01	0.71	4.41	14q22.3
15	205239_at	AREG	4.09	8.41E-05	2.40E-01	0.65	4.36	4q13-q21
16	222621_at	DNAJC1	1.74	1.91E-04	2.80E-01	0.67	4.33	10p12.31
17	201015_s_at	JUP	5.12	9.08E-05	2.40E-01	0.64	4.33	17q21

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
18	215356_at	FLJ13072	-1.69	6.97E-04	3.52E-01	-0.79	-4.31	19q12
19	228058_at	LOC124220	2.88	1.44E-04	2.68E-01	0.65	4.30	16p13.3
20	203056_s_at	PRDM2	1.83	1.02E-04	2.40E-01	0.63	4.29	1p36
21	231561_s_at	APOC2	-1.64	3.01E-04	2.80E-01	-0.69	-4.28	19q13.2
22	215411_s_at	C6orf4	1.50	1.50E-04	2.68E-01	0.64	4.28	6q21
23	225337_at	VAPA	1.95	1.03E-04	2.40E-01	0.62	4.27	18p11.21
24	213620_s_at	ICAM2	1.87	1.15E-04	2.54E-01	0.63	4.26	17q23-q25
25	206281_at	ADCYAP1	-1.32	2.46E-04	2.80E-01	-0.67	-4.26	18p11
26	211997_x_at	H3F3B	1.36	3.46E-04	2.88E-01	0.69	4.26	17q25
27	211503_s_at	RAB14	1.41	1.25E-04	2.60E-01	0.62	4.22	9q32-q34.11
28	236277_at		-2.81	1.15E-03	3.73E-01	-0.84	-4.21	
29	232977_x_at	FLJ13881	-1.68	6.26E-04	3.44E-01	-0.72	-4.19	19q13.33
30	203183_s_at	SMARCD1	1.34	2.21E-04	2.80E-01	0.63	4.17	12q13-q14
31	228384_s_at	MGC13047	2.58	1.63E-04	2.77E-01	0.60	4.13	10q24.2
32	212871_at	MAPKAPK5	1.33	2.76E-04	2.80E-01	0.63	4.11	12q24.13
33	205997_at	ADAM28	2.57	2.23E-04	2.80E-01	0.61	4.10	8p21.1
34	212385_at		2.45	2.32E-04	2.80E-01	0.61	4.09	
35	210706_s_at	RNF24	1.59	1.79E-04	2.80E-01	0.60	4.09	20p13-p12.1
36	220981_x_at	NXF2	-1.53	3.45E-04	2.88E-01	-0.62	-4.05	Xq22-q23
37	212249_at	PIK3R1	1.96	2.04E-04	2.80E-01	0.59	4.05	5q12-q13
38	226895_at	GEMIN7	1.58	6.05E-04	3.38E-01	0.66	4.04	19q13.32
39	214966_at	GRIK5	2.53	2.48E-04	2.80E-01	0.60	4.04	19q13.2
40	231479_at		-2.24	5.93E-04	3.38E-01	-0.65	-4.02	
41	215997_s_at	CUL4B	1.38	2.50E-04	2.80E-01	0.59	4.01	Xq23
42	226109_at	C21orf91	2.13	3.08E-04	2.80E-01	0.60	4.01	21q21.1
43	234160_at		-1.88	8.61E-04	3.59E-01	-0.66	-3.96	
44	210665_at	TFPI	3.94	2.83E-04	2.80E-01	0.58	3.96	2q31-q32.1
45	210664_s_at	TFPI	2.96	3.01E-04	2.80E-01	0.58	3.95	2q31-q32.1
46	203618_at	FAIM2	-1.29	9.01E-04	3.59E-01	-0.66	-3.95	12q13
47	202135_s_at	ACTR1B	1.42	2.92E-04	2.80E-01	0.58	3.95	2q11.1-q11.2
48	206412_at	FER	2.56	2.97E-04	2.80E-01	0.57	3.92	5q21
49	209099_x_at	JAG1	2.30	2.99E-04	2.80E-01	0.57	3.92	20p12.1-p11.23
50	225238_at		2.63	3.04E-04	2.80E-01	0.57	3.92	

6.17 AML M4 versus AML M5b

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	204169_at	IMPDH1	-1.82	8.97E-08	1.46E-03	-1.07	-7.12	7q31.3-q32
2	204158_s_at	TCIRG1	-1.80	5.10E-08	1.46E-03	-0.94	-6.67	11q13.4-q13.5
3	204620_s_at	CSPG2	-2.32	1.30E-07	1.46E-03	-0.92	-6.46	5q14.3
4	221731_x_at	CSPG2	-2.29	1.80E-07	1.51E-03	-0.88	-6.25	5q14.3
5	235109_at		4.73	3.83E-07	2.57E-03	0.81	5.86	

#	Probe	Gene						
6	228974_at		2.53	6.72E-07	3.67E-03	0.79	5.72	
7	229860_x_at		-1.65	3.17E-06	5.92E-03	-0.85	-5.72	
8	200953_s_at	CCND2	2.44	7.65E-07	3.67E-03	0.80	5.70	12p13
9	202388_at	RGS2	-1.60	9.83E-07	4.13E-03	-0.78	-5.63	1q31
10	200678_x_at	GRN	-1.91	2.10E-06	5.77E-03	-0.80	-5.59	17q21.32
11	210664_s_at	TFPI	4.27	2.23E-06	5.77E-03	0.81	5.53	2q31-q32.1
12	212501_at	CEBPB	-1.56	2.73E-06	5.77E-03	-0.78	-5.49	20q13.1
13	204398_s_at	EML2	-1.50	3.57E-06	6.31E-03	-0.78	-5.46	19q13.32
14	224719_s_at	LOC113246	1.66	1.65E-06	5.77E-03	0.74	5.42	12p13.31
15	205786_s_at	ITGAM	-1.86	2.62E-06	5.77E-03	-0.76	-5.41	16p11.2
16	213016_at		2.03	1.72E-06	5.77E-03	0.74	5.41	
17	216262_s_at	TGIF2	1.67	1.89E-06	5.77E-03	0.74	5.38	20q11.2-q12
18	217733_s_at	TMSB10	-1.29	5.29E-06	7.95E-03	-0.76	-5.33	2p11.2
19	216041_x_at	GRN	-1.88	4.55E-06	7.30E-03	-0.75	-5.29	17q21.32
20	201161_s_at	CSDA	1.76	2.75E-06	5.77E-03	0.73	5.28	12p13.1
21	205964_at	MGC2663	1.94	2.93E-06	5.80E-03	0.72	5.27	19p13.2
22	213702_x_at	ASAH1	-1.52	1.60E-05	1.21E-02	-0.78	-5.17	8p22-p21.3
23	228402_at	MGC15435	2.08	6.75E-06	8.96E-03	0.74	5.15	5q13.2
24	200951_s_at	CCND2	2.82	4.35E-06	7.30E-03	0.71	5.15	12p13
25	211284_s_at	GRN	-1.99	8.35E-06	9.64E-03	-0.73	-5.15	17q21.32
26	203574_at	NFIL3	-1.58	7.50E-06	9.35E-03	-0.71	-5.09	9q22
27	234339_s_at	GLTSCR2	1.75	1.23E-05	1.06E-02	0.73	5.08	19q13.3
28	90265_at	CENTA1	-1.62	2.00E-05	1.37E-02	-0.76	-5.08	7p22.3
29	209862_s_at	KIAA0092	1.49	5.44E-06	7.95E-03	0.70	5.08	11q21
30	224841_x_at		1.50	9.07E-06	9.64E-03	0.71	5.06	
31	205180_s_at	ADAM8	-1.70	9.30E-06	9.64E-03	-0.71	-5.06	10q26.3
32	200871_s_at	PSAP	-1.53	8.52E-06	9.64E-03	-0.71	-5.05	10q21-q22
33	201954_at	ARPC1B	-1.65	2.26E-05	1.43E-02	-0.76	-5.05	7q22.1
34	225698_at	TIGA1	1.64	6.57E-06	8.96E-03	0.69	5.03	5q21-q22
35	202732_at	PKIG	1.93	6.92E-06	8.96E-03	0.69	5.02	20q12-q13.1
36	214351_x_at	RPL13	1.26	9.05E-06	9.64E-03	0.69	5.00	16q24.3
37	205756_s_at	F8	-1.66	3.50E-05	1.55E-02	-0.76	-4.98	Xq28
38	210184_at	ITGAX	-2.11	2.73E-05	1.47E-02	-0.75	-4.98	16p11.2
39	200985_s_at	CD59	2.73	1.19E-05	1.06E-02	0.70	4.94	11p13
40	208438_s_at	FGR	-2.05	2.54E-05	1.45E-02	-0.73	-4.93	1p36.2-p36.1
41	203588_s_at	TFDP2	2.65	1.22E-05	1.06E-02	0.70	4.93	3q23
42	201944_at	HEXB	-1.83	3.31E-05	1.51E-02	-0.74	-4.93	5q13
43	234660_s_at	DIS3	1.58	9.46E-06	9.64E-03	0.68	4.92	13q21.32
44	224741_x_at		1.51	1.48E-05	1.16E-02	0.69	4.92	
45	210993_s_at	MADH1	2.36	1.11E-05	1.06E-02	0.68	4.91	4q28
46	220688_s_at	C1orf33	1.98	1.06E-05	1.05E-02	0.67	4.90	1p36.13
47	214084_x_at	NCF1	-2.84	5.19E-05	1.73E-02	-0.77	-4.90	7q11.23
48	229050_s_at		1.75	1.20E-05	1.06E-02	0.68	4.89	
49	200074_s_at - HG-U133A	RPL14	1.22	1.98E-05	1.37E-02	0.70	4.88	3p22-p21.2

50	200743_s_at	CLN2	-1.45	3.10E-05	1.51E-02	-0.72	-4.86	11p15

6.18 AML M4 versus AML M6

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	211070_x_at	DBI	3.31	2.14E-14	3.06E-10	1.68	11.27	2q12-q21
2	202428_x_at	DBI	2.98	2.29E-14	3.06E-10	1.67	11.23	2q12-q21
3	201105_at	LGALS1	14.95	2.02E-11	1.80E-07	1.53	9.59	22q13.1
4	209389_x_at	DBI	2.49	3.14E-11	2.10E-07	1.38	9.19	2q12-q21
5	221666_s_at	ASC	5.54	2.06E-10	1.10E-06	1.25	8.34	16p12-p11.2
6	58780_s_at	FLJ10357	3.97	3.83E-10	1.71E-06	1.21	8.08	14q11.1
7	224916_at		4.00	1.21E-09	3.01E-06	1.22	7.97	
8	224983_at		2.66	7.93E-10	3.01E-06	1.18	7.90	
9	217226_s_at	BA108L7.2	3.38	1.05E-09	3.01E-06	1.19	7.89	10q24.31
10	208717_at	OXA1L	1.81	1.11E-09	3.01E-06	1.17	7.82	14q11.2
11	200652_at	SSR2	1.92	6.51E-09	7.23E-06	1.19	7.78	1q21-q23
12	229860_x_at		3.37	7.15E-08	3.33E-05	1.23	7.71	
13	223718_at	ACRBP	3.99	1.24E-09	3.01E-06	1.15	7.71	12p13.31
14	208659_at	CLIC1	1.75	6.76E-09	7.23E-06	1.16	7.64	6p22.1-p21.2
15	213870_at	COL11A2	3.79	1.83E-09	4.07E-06	1.14	7.62	6p21.3
16	224929_at		2.94	2.88E-09	5.41E-06	1.14	7.56	
17	201259_s_at	SYPL	1.92	2.98E-09	5.41E-06	1.13	7.55	7q22.1
18	232032_x_at	Cab45	2.12	7.59E-08	3.33E-05	1.18	7.49	1p36.33
19	201231_s_at	ENO1	2.03	3.85E-08	2.51E-05	1.16	7.47	1p36.3-p36.2
20	212431_at	KIAA0194	2.14	7.44E-08	3.33E-05	1.18	7.46	5q33.1
21	225045_at	FLJ10392	4.04	1.56E-08	1.30E-05	1.14	7.44	2p16.1
22	221581_s_at	WBSCR5	2.92	3.03E-09	5.41E-06	1.11	7.44	7q11.23
23	213185_at	KIAA0556	1.50	5.27E-09	6.58E-06	1.11	7.42	16p12.1
24	216015_s_at	CIAS1	6.99	5.04E-09	6.58E-06	1.12	7.42	1q44
25	209876_at	GIT2	2.99	1.06E-08	9.82E-06	1.12	7.39	12q24.1
26	228415_at	AP1S2	2.57	4.79E-09	6.58E-06	1.11	7.38	Xp22.31
27	220326_s_at	FLJ10357	3.57	4.26E-09	6.58E-06	1.10	7.38	14q11.1
28	224374_s_at	EMILIN-2	3.19	3.73E-09	6.23E-06	1.10	7.37	18p11.3
29	225605_at	LOC90313	5.13	4.93E-09	6.58E-06	1.10	7.35	17q11.1
30	223640_at	PIK3AP	2.62	1.02E-08	9.72E-06	1.10	7.31	19q13.1
31	227268_at	LOC51136	2.62	5.41E-09	6.58E-06	1.08	7.26	17q23.2
32	238996_x_at	ALDOA	2.16	8.23E-09	8.16E-06	1.09	7.26	16q22-q24
33	32837_at	AGPAT2	1.88	6.21E-08	3.33E-05	1.13	7.25	9q34.3
34	235022_at	MGC24180	2.15	5.88E-09	6.84E-06	1.08	7.24	18p11.1
35	224455_s_at	DKFZP434B195	3.57	1.20E-08	1.07E-05	1.08	7.18	15q22.33
36	208764_s_at	ATP5G2	1.90	2.21E-07	5.80E-05	1.14	7.17	12q13.13
37	221710_x_at	FLJ10647	3.71	8.03E-09	8.16E-06	1.07	7.17	1p34.3
38	220974_x_at	BA108L7.2	5.50	1.24E-08	1.07E-05	1.08	7.14	10q24.31

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
39	201061_s_at	STOM	-2.26	6.27E-06	4.62E-04	-1.27	-7.06	9q34.1
40	229841_at		-1.70	1.18E-07	4.40E-05	-1.10	-7.06	
41	205442_at	KIAA0626	-3.50	1.42E-05	8.05E-04	-1.33	-7.04	4q32.3
42	201136_at	PLP2	2.24	1.83E-08	1.40E-05	1.05	7.02	Xp11.23
43	201647_s_at	SCARB2	1.96	1.80E-07	5.30E-05	1.10	6.99	4q21.1
44	223156_at	MRPS23	2.00	2.43E-08	1.63E-05	1.04	6.95	17q22-q23
45	201487_at	CTSC	2.76	1.80E-08	1.40E-05	1.04	6.94	11q14.1-q14.3
46	209500_x_at	TNFSF13	3.26	1.78E-08	1.40E-05	1.04	6.92	17p13.1
47	210493_s_at	KIAA0626	-2.42	1.38E-05	7.87E-04	-1.29	-6.92	4q32.3
48	225214_at		2.48	2.30E-08	1.62E-05	1.04	6.91	
49	200946_x_at	GLUD1	2.00	7.92E-08	3.42E-05	1.05	6.86	10q23.3
50	224747_at	LOC92912	1.87	2.06E-08	1.53E-05	1.02	6.86	15q23

6.19	AML M5a versus AML M5b							

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	243720_at		2.92	1.23E-04	1.94E-01	1.14	5.31	
2	216041_x_at	GRN	-2.14	3.18E-05	1.48E-01	-1.00	-5.20	17q21.32
3	219452_at	LOC64174	-3.18	2.12E-05	1.48E-01	-0.99	-5.20	16q22.1
4	228058_at	LOC124220	-3.40	2.02E-05	1.48E-01	-0.98	-5.20	16p13.3
5	204184_s_at	ADRBK2	-1.71	2.72E-05	1.48E-01	-0.98	-5.13	22q12.1
6	200678_x_at	GRN	-2.09	4.07E-05	1.48E-01	-0.99	-5.11	17q21.32
7	236916_at		1.55	2.73E-05	1.48E-01	0.96	5.08	
8	211284_s_at	GRN	-2.17	4.05E-05	1.48E-01	-0.96	-5.02	17q21.32
9	201360_at	CST3	-2.34	1.07E-04	1.94E-01	-1.00	-4.99	20p11.21
10	214908_s_at	TRRAP	2.15	3.80E-05	1.48E-01	0.94	4.97	7q21.2-q22.1
11	229957_at		-2.32	4.18E-05	1.48E-01	-0.94	-4.94	
12	225373_at	PP2135	-2.33	4.79E-05	1.52E-01	-0.93	-4.92	10q22.3
13	235568_at	LOC199675	-3.82	9.81E-05	1.94E-01	-0.93	-4.76	19p13.2
14	226810_at		-2.93	1.03E-04	1.94E-01	-0.93	-4.75	
15	238469_at		-2.10	7.40E-05	1.94E-01	-0.90	-4.73	
16	227131_at	MGC10986	-1.87	8.10E-05	1.94E-01	-0.89	-4.68	17q24.1
17	205922_at	VNN2	-5.74	1.45E-04	1.94E-01	-0.93	-4.68	6q23-q24
18	224560_at	TIMP2	-2.30	8.90E-05	1.94E-01	-0.88	-4.64	17q25
19	212807_s_at	SORT1	-2.36	1.20E-04	1.94E-01	-0.88	-4.62	1p21.3-p13.1
20	226678_at		-2.26	1.32E-04	1.94E-01	-0.86	-4.53	
21	38487_at	STAB1	-2.63	1.29E-04	1.94E-01	-0.85	-4.50	3p21.31
22	227037_at	LOC201164	1.52	6.48E-04	2.66E-01	1.00	4.50	17p11.2
23	200808_s_at	ZYX	-1.79	1.47E-04	1.94E-01	-0.85	-4.49	7q32
24	206393_at	TNNI2	-2.84	1.32E-04	1.94E-01	-0.85	-4.48	11p15.5
25	224801_at	NDFIP2	1.76	5.68E-04	2.60E-01	0.96	4.47	13q22.1
26	228532_at	MGC24133	-2.33	1.57E-04	1.94E-01	-0.85	-4.46	1p13.1
27	221541_at	DKFZP434B044	-3.02	1.43E-04	1.94E-01	-0.84	-4.45	16q24.1

#	affy id	HUGO name						
28	202682_s_at	USP4	-1.43	1.60E-04	1.94E-01	-0.83	-4.41	3p21.3
29	209500_x_at	TNFSF13	-2.13	1.65E-04	1.94E-01	-0.83	-4.40	17p13.1
30	243769_at		1.90	5.28E-04	2.60E-01	0.92	4.40	
31	225940_at	MGC39820	-2.69	1.87E-04	2.12E-01	-0.83	-4.36	3p14
32	224525_s_at	PTD004	2.29	4.38E-04	2.59E-01	0.88	4.35	2q31.1
33	237283_at		2.32	5.83E-04	2.60E-01	0.90	4.34	
34	226895_at	GEMIN7	-1.66	2.68E-04	2.22E-01	-0.83	-4.33	19q13.32
35	231579_s_at	TIMP2	-2.04	2.17E-04	2.22E-01	-0.82	-4.33	17q25
36	204183_s_at	ADRBK2	-1.74	2.74E-04	2.22E-01	-0.83	-4.31	22q12.1
37	235322_at	LOC148189	1.62	3.97E-04	2.47E-01	0.85	4.29	19q11
38	205382_s_at	DF	-1.71	2.81E-04	2.22E-01	-0.82	-4.29	19p13.3
39	207600_at	KCNC3	1.73	2.75E-04	2.22E-01	0.82	4.29	19q13.3-q13.4
40	216511_s_at		-2.57	2.30E-04	2.22E-01	-0.81	-4.28	
41	211250_s_at	SH3BP2	-1.69	2.40E-04	2.22E-01	-0.81	-4.26	4p16.3
42	226841_at	LOC219972	-2.97	2.41E-04	2.22E-01	-0.81	-4.26	11q12.1
43	210580_x_at	SULT1A3	-2.17	3.59E-04	2.43E-01	-0.84	-4.25	16p11.2
44	205844_at	VNN1	-5.53	4.50E-04	2.59E-01	-0.87	-4.25	6q23-q24
45	225941_at	MGC39820	-2.51	2.49E-04	2.22E-01	-0.80	-4.24	3p14
46	217614_at		-1.48	2.84E-04	2.22E-01	-0.81	-4.23	
47	205931_s_at	H_GS165L15.1	-2.35	2.65E-04	2.22E-01	-0.80	-4.22	7p15
48	228094_at	AMICA	-6.72	5.16E-04	2.60E-01	-0.87	-4.21	11q23.3
49	217921_at		-1.51	2.84E-04	2.22E-01	-0.80	-4.21	
50	206420_at	IGSF6	-3.20	4.63E-04	2.59E-01	-0.85	-4.21	16p12-p13

6.20 AML M5a versus AML M6

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	205442_at	KIAA0626	-3.19	1.98E-05	1.43E-01	-1.52	-6.48	4q32.3
2	229898_at		-2.76	2.15E-05	1.43E-01	-1.36	-5.98	
3	32259_at	EZH1	-2.03	1.74E-05	1.43E-01	-1.32	-5.87	17q21.1-q21.3
4	202025_x_at	ACAA1	1.51	3.16E-05	1.43E-01	1.34	5.84	3p23-p22
5	214733_s_at	DJ167A19.1	1.64	2.58E-05	1.43E-01	1.32	5.79	1p33-p32.1
6	232181_at		3.50	5.35E-05	1.43E-01	1.37	5.79	
7	74694_s_at	FRA	1.88	4.18E-05	1.43E-01	1.31	5.69	16p12.1
8	213587_s_at	LOC155066	2.95	7.77E-05	1.58E-01	1.33	5.62	7q36.1
9	207675_x_at	ARTN	2.45	4.32E-05	1.43E-01	1.28	5.61	1p33-p32
10	209320_at	ADCY3	1.84	6.20E-05	1.45E-01	1.31	5.61	2p24-p22
11	219255_x_at	IL17BR	1.94	4.81E-05	1.43E-01	1.29	5.61	3p21.1
12	230413_s_at	AP1S2	3.81	1.40E-04	2.09E-01	1.40	5.59	Xp22.31
13	208174_x_at	U2AF1RS2	1.75	4.86E-05	1.43E-01	1.28	5.57	Xp22.1
14	217931_at	TNRC5	1.93	4.02E-05	1.43E-01	1.22	5.44	6pter-p12.1
15	206117_at	TPM1	-3.22	8.90E-05	1.58E-01	-1.25	-5.41	15q22.1
16	90610_at	LRRN1	1.65	5.20E-05	1.43E-01	1.21	5.37	7q22
17	210907_s_at	PDCD10	-1.59	4.51E-05	1.43E-01	-1.19	-5.34	3q26.2

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
18	212430_at	RNPC1	-2.88	5.21E-05	1.43E-01	-1.19	-5.30	20q13.31
19	214805_at		1.88	7.70E-05	1.58E-01	1.21	5.29	
20	223754_at	MGC13057	-5.31	3.08E-04	2.49E-01	-1.30	-5.25	2q32.3
21	221581_s_at	WBSCR5	2.88	2.08E-04	2.44E-01	1.28	5.23	7q11.23
22	218434_s_at	FLJ12389	2.11	6.16E-05	1.45E-01	1.17	5.22	12q24.31
23	206698_at	XK	-6.40	5.00E-04	2.49E-01	-1.38	-5.22	Xp21.1
24	217984_at	RNASE6PL	2.55	9.14E-05	1.58E-01	1.17	5.16	6q27
25	201561_s_at	CLSTN1	2.55	2.21E-04	2.44E-01	1.23	5.10	1p36.22
26	205059_s_at	IDUA	1.89	8.77E-05	1.58E-01	1.13	5.05	4p16.3
27	221080_s_at	FLJ22757	1.77	9.27E-05	1.58E-01	1.13	5.02	19p13.3
28	204269_at	PIM2	-1.51	1.01E-04	1.64E-01	-1.11	-4.97	Xp11.23
29	212343_at		-3.55	4.71E-04	2.49E-01	-1.23	-4.96	
30	205211_s_at	RIN1	2.02	1.68E-04	2.29E-01	1.13	4.94	11q13.1
31	223928_s_at	GUCA1C	-1.97	1.29E-04	2.01E-01	-1.08	-4.85	3q13.1
32	206994_at	CST4	2.51	1.91E-04	2.44E-01	1.10	4.83	20p11.21
33	220252_x_at	FLJ11577	2.83	1.51E-04	2.18E-01	1.08	4.82	Xp21.3
34	207930_at	LCN1	2.14	1.71E-04	2.29E-01	1.08	4.80	9q34
35	223562_at	PARVG	2.86	4.04E-04	2.49E-01	1.16	4.79	22q13.2-q13
36	222017_x_at	LRRN1	1.96	2.52E-04	2.49E-01	1.10	4.78	7q22
37	203544_s_at	STAM	-2.73	7.24E-04	2.49E-01	-1.21	-4.78	10p14-p13
38	218779_x_at	EPS8R1	2.95	2.10E-04	2.44E-01	1.09	4.77	19q13.42
39	32837_at	AGPAT2	1.85	2.87E-04	2.49E-01	1.09	4.72	9q34.3
40	227738_s_at	FLJ13063	1.87	2.60E-04	2.49E-01	1.07	4.71	16p11.2
41	224698_at	KIAA1228	2.68	2.77E-04	2.49E-01	1.08	4.70	7q36.3
42	201944_at	HEXB	2.79	6.55E-04	2.49E-01	1.20	4.68	5q13
43	201061_s_at	STOM	-2.24	2.15E-04	2.44E-01	-1.05	-4.67	9q34.1
44	204848_x_at	HBG1	-2.83	1.98E-04	2.44E-01	-1.04	-4.65	11p15.5
45	243691_at		-3.59	3.11E-04	2.49E-01	-1.06	-4.64	
46	205919_at	HBE1	-4.36	4.78E-04	2.49E-01	-1.08	-4.62	11p15.5
47	208759_at	NCSTN	1.70	3.08E-04	2.49E-01	1.06	4.62	1q22-q23
48	206871_at	ELA2	-2.75	2.30E-04	2.46E-01	-1.03	-4.61	19p13.3
49	218592_s_at	CECR5	3.50	6.12E-04	2.49E-01	1.13	4.61	
50	214219_x_at	MAP4K1	3.18	3.06E-04	2.49E-01	1.05	4.61	19q13.1-q13.4

6.21 AML M5b versus AML M6

#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	35820_at	GM2A	5.96	2.72E-11	2.02E-07	2.36	11.94	5q31.3-q33.1
2	201590_x_at	ANXA2	6.32	2.64E-11	2.02E-07	2.31	11.72	15q21-q22
3	229860_x_at		5.56	2.58E-11	2.02E-07	2.27	11.59	
4	210427_x_at	ANXA2	5.95	3.33E-11	2.02E-07	2.26	11.51	15q21-q22
5	213503_x_at	ANXA2	6.16	6.48E-11	2.62E-07	2.21	11.23	15q21-q22
6	204620_s_at	CSPG2	9.60	6.02E-11	2.62E-07	2.19	11.14	5q14.3

7	221731_x_at	CSPG2	10.05	8.48E-11	2.95E-07	2.15	10.94	5q14.3
8	201360_at	CST3	7.62	2.70E-10	7.29E-07	2.12	10.72	20p11.21
9	216041_x_at	GRN	5.36	1.86E-10	5.66E-07	2.10	10.66	17q21.32
10	204057_at	ICSBP1	5.21	4.22E-10	9.32E-07	2.05	10.36	16q24.1
11	211284_s_at	GRN	5.72	1.19E-09	2.07E-06	2.08	10.32	17q21.32
12	200678_x_at	GRN	4.63	3.76E-10	9.14E-07	2.01	10.22	17q21.32
13	201105_at	LGALS1	20.11	2.15E-08	1.21E-05	2.32	10.09	22q13.1
14	218217_at	RISC	6.51	9.86E-10	1.85E-06	2.00	10.07	17q23.1
15	203574_at	NFIL3	3.15	9.87E-10	1.85E-06	1.95	9.90	9q22
16	212737_at	GM2A	4.09	1.95E-09	2.79E-06	1.90	9.60	5q31.3-q33.1
17	211070_x_at	DBI	4.15	1.87E-08	1.13E-05	2.01	9.53	2q12-q21
18	208659_at	CLIC1	1.91	1.63E-09	2.47E-06	1.87	9.51	6p22.1-p21.2
19	203973_s_at	CEBPD	4.77	7.09E-09	6.15E-06	1.89	9.47	8p11.2-p11.1
20	201944_at	HEXB	4.34	2.11E-08	1.21E-05	2.00	9.46	5q13
21	209166_s_at	MAN2B1	3.24	1.52E-09	2.47E-06	1.86	9.45	19cen-q13.1
22	202363_at	SPOCK	3.93	6.91E-09	6.15E-06	1.88	9.41	5q31
23	226276_at	LOC153339	3.45	7.93E-09	6.65E-06	1.89	9.33	5q14.1
24	215075_s_at	GRB2	2.36	2.23E-09	3.01E-06	1.81	9.25	17q24-q25
25	219150_s_at	CENTA1	9.07	5.40E-08	1.99E-05	2.03	9.23	7p22.3
26	201127_s_at	ACLY	2.55	1.81E-08	1.13E-05	1.86	9.22	17q12-q21
27	210549_s_at	CCL23	29.53	6.60E-08	2.17E-05	2.06	9.20	17q12
28	220326_s_at	FLJ10357	4.82	6.61E-09	6.15E-06	1.84	9.19	14q11.1
29	202428_x_at	DBI	3.78	3.05E-08	1.50E-05	1.93	9.18	2q12-q21
30	211612_s_at	IL13RA1	3.99	2.67E-09	3.42E-06	1.80	9.16	Xq24
31	209619_at	CD74	3.13	2.37E-08	1.28E-05	1.84	9.11	5q32
32	216274_s_at	SPC18	2.11	3.11E-09	3.78E-06	1.79	9.11	15q24.3
33	225605_at	LOC90313	5.80	1.54E-08	1.07E-05	1.84	9.06	17q11.1
34	217733_s_at	TMSB10	1.78	1.61E-08	1.07E-05	1.80	9.02	2p11.2
35	221581_s_at	WBSCR5	4.10	2.36E-08	1.28E-05	1.85	9.00	7q11.23
36	210524_x_at	MT1F	3.09	1.17E-08	8.65E-06	1.80	8.98	16q13
37	202877_s_at	C1QR1	5.73	5.55E-09	5.87E-06	1.76	8.94	20p11.21
38	208683_at	CAPN2	4.26	5.00E-09	5.79E-06	1.76	8.93	1q41-q42
39	202803_s_at	ITGB2	3.53	1.82E-07	3.86E-05	1.86	8.92	21q22.3
40	218218_at	DIP13B	-1.68	7.01E-09	6.15E-06	-1.75	-8.85	12q24.1
41	211986_at	AHNAK	8.49	4.45E-08	1.82E-05	1.84	8.83	11q12-q13
42	224846_at	LOC92799	4.57	5.29E-09	5.84E-06	1.73	8.83	19q13.13
43	221841_s_at		5.05	3.26E-08	1.50E-05	1.77	8.82	
44	210872_x_at	GAS7	3.37	8.64E-09	7.00E-06	1.74	8.80	17p
45	204502_at	SAMHD1	8.49	3.77E-08	1.67E-05	1.81	8.77	20pter-q12
46	208890_s_at	PLXNB2	5.08	6.66E-09	6.15E-06	1.72	8.74	22q13.33
47	201186_at	LRPAP1	4.56	7.03E-08	2.27E-05	1.83	8.70	4p16.3
48	212430_at	RNPC1	-4.98	8.42E-06	4.06E-04	-2.13	-8.66	20q13.31
49	209500_x_at	TNFSF13	5.30	8.13E-08	2.56E-05	1.83	8.65	17p13.1
50	202192_s_at	GAS7	4.02	1.13E-08	8.56E-06	1.71	8.65	17p

Table 7

7. One-Versus-All (OVA)							
7.1 AML M3 versus M3M3V							
#	affy id	HUGO name	fc	p	q	stn	t	Map Location
1	217854_s_at	POLR2E	-2.33	4.76E-08	1.44E-03	-2.06	-9.15	19p13.3
2	200916_at	TAGLN2	-2.81	2.03E-07	3.08E-03	-1.92	-8.49	1q21-q25
3	200872_at	S100A10	-3.70	3.53E-06	2.68E-02	-2.02	-8.25	1q21
4	201105_at	LGALS1	-5.65	1.36E-06	1.37E-02	-1.73	-7.57	22q13.1
5	200758_s_at	NFE2L1	-2.22	1.54E-05	3.73E-02	-1.63	-6.80	17q21.3
6	218291_at	HSPC003	-1.97	1.91E-05	3.73E-02	-1.64	-6.78	1q21.3
7	201590_x_at	ANXA2	-2.03	4.86E-06	2.95E-02	-1.54	-6.76	15q21-q22
8	210427_x_at	ANXA2	-2.02	1.10E-05	3.73E-02	-1.55	-6.64	15q21-q22
9	208690_s_at	PDLIM1	-2.86	2.38E-05	3.73E-02	-1.58	-6.57	10q22-q26.3
10	213503_x_at	ANXA2	-2.01	8.26E-06	3.73E-02	-1.46	-6.42	15q21-q22
11	202331_at	BCKDHA	-2.26	8.88E-06	3.73E-02	-1.44	-6.36	19q13.1-q13.2
12	227592_at	MGC10204	-5.48	5.02E-05	4.19E-02	-1.54	-6.27	19q13.33
13	216397_s_at	BOP1	-1.69	1.11E-05	3.73E-02	-1.42	-6.25	8q24.3
14	203186_s_at	S100A4	-2.86	2.96E-05	3.73E-02	-1.39	-6.01	1q21
15	222557_at	STMN3	-2.31	8.73E-05	4.91E-02	-1.46	-5.92	20q13.3
16	234797_at		1.54	1.46E-05	3.73E-02	1.32	5.91	
17	232583_at		3.16	2.14E-05	3.73E-02	1.34	5.90	
18	203150_at	RAB9P40	-1.90	3.03E-05	3.73E-02	-1.36	-5.90	9q34.11
19	202009_at	PTK9L	-2.26	3.38E-05	3.73E-02	-1.36	-5.88	3p21.1
20	201245_s_at	FLJ20113	-1.63	1.51E-05	3.73E-02	-1.31	-5.86	11q12.3
21	213330_s_at	STIP1	-2.94	3.14E-05	3.73E-02	-1.33	-5.83	11q13
22	201651_s_at	PACSIN2	-3.09	2.80E-05	3.73E-02	-1.32	-5.80	22q13.2-13.33
23	229860_x_at		-2.11	3.44E-05	3.73E-02	-1.30	-5.69	
24	201954_at	ARPC1B	-2.27	4.40E-05	4.12E-02	-1.31	-5.69	7q22.1
25	200034_s_at - HG-U133A	RPL6	1.17	2.45E-05	3.73E-02	1.28	5.68	12q24.1
26	203832_at	SNRPF	-1.95	4.48E-05	4.12E-02	-1.31	-5.68	12q23.1
27	243_g_at	MAP4	-1.89	2.80E-05	3.73E-02	-1.28	-5.66	3p21
28	200076_s_at - HG-U133B	MGC2749	-1.89	1.48E-04	5.82E-02	-1.41	-5.65	19p13.11
29	218473_s_at	FLJ22329	-2.12	3.70E-05	3.80E-02	-1.27	-5.61	19p13.11
30	224312_x_at	FLJ20542	-1.99	1.68E-04	5.93E-02	-1.40	-5.60	1p36.33
31	205081_at	CRIP1	-15.08	2.86E-04	7.28E-02	-1.55	-5.59	7q11.23
32	209224_s_at	NDUFA2	-1.54	2.85E-05	3.73E-02	-1.25	-5.59	5q31
33	222644_s_at	FLJ22329	-2.33	3.76E-05	3.80E-02	-1.26	-5.58	19p13.11
34	218317_x_at	MGC5178	-1.92	3.40E-05	3.73E-02	-1.25	-5.55	16p12.1
35	225605_at	LOC90313	-3.65	9.57E-05	5.06E-02	-1.30	-5.52	17q11.1
36	216591_s_at		-2.46	6.55E-05	4.78E-02	-1.28	-5.52	
37	221800_s_at	FLJ22175	-1.91	8.11E-05	4.91E-02	-1.28	-5.50	
38	223244_s_at	DAP13	-1.53	3.23E-05	3.73E-02	-1.23	-5.49	12q21.33
39	211730_s_at	POLR2L	-1.95	3.25E-05	3.73E-02	-1.23	-5.49	11p15
40	202564_x_at	ARL2	-2.46	5.65E-05	4.52E-02	-1.25	-5.48	11q13

41	209303_at	NDUFS4	-1.48	3.34E-05	3.73E-02	-1.23	-5.48	5q11.1
42	202218_s_at	FADS2	-2.29	5.08E-05	4.19E-02	-1.23	-5.43	11q12-q13.1
43	226437_at	LOC90522	-1.69	4.38E-05	4.12E-02	-1.21	-5.38	19q13.13
44	244065_at		2.66	5.11E-05	4.19E-02	1.21	5.37	
45	228014_at	LOC138428	-2.50	8.64E-05	4.91E-02	-1.24	-5.36	9q34.12
46	233625_x_at	FLJ20542	-1.79	5.93E-05	4.61E-02	-1.21	-5.35	1p36.33
47	205115_s_at	KIAA0682	-1.71	1.48E-04	5.82E-02	-1.26	-5.32	12q24.21
48	209229_s_at	KIAA1115	-1.74	8.20E-05	4.91E-02	-1.21	-5.30	19q13.42
49	200946_x_at	GLUD1	-1.80	6.71E-05	4.78E-02	-1.20	-5.29	10q23.3
50	202785_at	NDUFA7	-1.57	5.11E-05	4.19E-02	-1.18	-5.28	19p13.2

Claims

1.   A method for distinguishing WHO classified AML subtypes AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a, AML_M5b, AML_M6, AML_t(15;17)/M3 and/or AML_t(15;17)/M3v in a sample, the method comprising determining the expression level of markers selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, 3, 4, 5, 6 and/or 7,

wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 1.1

is indicative for the presence of AML_MLL when AML_MLL is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 1.2

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from all other subtypes,

and/or wherein

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 1.3 and/or

a lower expression of at least one polynucleotide defined by any of the numbers 41 of Table 1.3

is indicative for the presence of AML_other when AML_other is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 1.4

is indicative for the presence of AML_t(15;17) when AML_t(15;17) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 1.5

is indicative for the presence of AML_t(8;21) when AML_t(8;21) is distinguished from all other subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 3, 4, 5, 6, 7, 11, 12, 13, 15, 16, 17, 19, 20, 22, 24, 25, 27, 28, 30, 31, 32, 33, 34, 35, 37, 41, 42, 43, 44, 46, 48, and/or 50 of Table 2.1, and or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 8, 9, 10, 14, 18, 21, 23, 26, 29, 36, 38, 39, 40, 45, 47, and/or 49 of Table 2.1,

is indicative for the presence of AML_MLL when AML_MLL is distinguished from AML_inv(16),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 2.2

is indicative for the presence of AML_MLL when AML_MLL is distinguished from AML_other,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 5, 6, 7, 8, 9, 11, 13, 15, 18, 20, 22, 24, 25, 26, 27, 29, 30, 33, 34, 35, 36, 41, 44, 46, , and/or 50 of Table 2.3, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 4, 10, 12, 14, 16, 17, 19, 21, 23, 28, 31, 32, 37, 38, 39, 40, 42, 43, 45, 47, 48, and/or 49 of Table 2.3

is indicative for the presence of AML_MLL when AML_MLL is distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 8, 13, 17, 18, 19, 23, 26, 27, 28, 29, 35, 38, 39, 40, 43, 45, and/or 50 of Table 2.4, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 9, 10, 11, 12, 14, 15, 16, 20, 21, 22, 24, 25, 30, 31, 32, 33, 34, 36, 37, 41, 42, 44, 46, 47, 48, and 49 of Table 2.4,

is indicative for the presence of AML_MLL when AML_MLL is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 2.5, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 37 of Table 2.5

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from AML_other,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 2, 4, 7, 9, 12, 17, 22, 23, 28, 29, 30, 34, 39, 42, and/or 49 of Table 2.6, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 3, 5, 6, 8, 10, 11, 13, 14, 15, 16, 18, 19, 20, 21, 24, 25, 26,

27, 31, 32, 33, 35, 36, 37, 38, 40, 41, 43, 44, 45, 46, 47, 48, and/or 50 of Table 2.6,

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from AML_t(15;17),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 6, 15, 27, 32, 36, 44, and/or 47, of Table 2.7, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 7, 8, 9, 10, 11, 12, 13, 14, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 28, 29, 30, 31, 33, 34, 35, 37, 38, 39, 40, 41, 42, 43, 45, 46, 48, 49, and/or 50 of Table 2.7,

is indicative for the presence of AML_inv(16) when AML_inv(16) is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 18, and/or 25 of Table 2.8, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 19, 20, 21, 22, 23, 24, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 2.8,

is indicative for AML_other when AML_other is distinguished from AML_t(15;17),

and/or wherein

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 2.9,

is indicative for AML_other when AML_other is distinguished from AML_t(8;21),

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 4, 7, 11, 14, 16, 18, 22, 23, 24, 25, 27, 29, 31, 32, 33, 36, 37, 38, 41, 42, 43, 47, 48, and/or 49, of Table 2.10,

a higher expression of at least one polynucleotide defined by any of the numbers 2, 3, 5, 6, 8, 9, 10, 12, 13, 15, 17, 19, 20, 21, 26, 28, 30, 34, 35, 39, 40, 44, 45, 46, and/or 50 of Table 2.10

is indicative for AML_t(15;17) when AML_t(15;17) is distinguished from AML_t(8;21),

and/or wherein

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 3.1,

is indicative for denovo_AML when denovo_AML is distinguished from all other AML subtypes

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 3.2,

is indicative for s_AML when s_AML is distinguished from all other AML subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 3.3,

is indicative for t_AML when t_AML is distinguished from all other AML subtypes

and/or wherein

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 4.1,

is indicative for denovo_AML when denovo_AML is distinguished from s_AML,

and/or wherein

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 4.2,

is indicative for denovo_AML when denovo_AML is distinguished from t_AML

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 7, 8, 12, 13, 15, 16, 17, 19, 21, 22, 23, 24, 25, 30, 31, 34, 35, 36, 37, 38, 41, 45, 47, and/or 50 of Table 4.3, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 9, 10, 11, 14, 18, 20, 26, 27, 28, 29, 32, 33, 39, 40, 42, 43, 44, 46, 48, and/or 49 of Table 4.3,

is indicative for s_AML when s_AML is distinguished from t_AML

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 5.1,

is indicative for AML_M0 when AML_M0 is distinguished from all other AML subtypes,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 5.2,

is indicative for AML_M1 when AML_M1 is distinguished from all other AML subtypes

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 33, 34, 35, 36, 37, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 5.3, and/or

5   a higher expression of at least one polynucleotide defined by any of the numbers 32 and/or 38 of Table 5.3

is indicative for AML_M2 when AML_M2 is distinguished from all other AML subtypes,

and/or wherein

10   a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 19, 20, 21, 22, 25, 26, 27, 29, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 5.4, and/or

a higher expression a polynucleotide defined by any of the numbers 18, 23, 24, 28, and/or 30 of Table 5.4

15   is indicative for AML_M4 when AML_M4 is distinguished from all other AML subtypes

and/or wherein

20   a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 5.5,

is indicative for AML_M5a when AML_M5a is distinguished from all other AML subtypes

25   and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 8, 9, 10, 11, 12, 13, 14, 15, 17, 18, 19, 21, 22, 23, 24, 25, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 39, 40, 42, 43, 44, 46, 48, 49, and/or 50 of Table 5.6, and/or

30   a higher expression of at least one polynucleotide defined by any of the numbers 6, 7, 16, 20, 26, 37, 38, 41, 45, and/or 47 of Table 5.6,

is indicative for AML_M5b when AML_M5b is distinguished from all other AML subtypes,

and/or wherein

5   a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 5.7,

is indicative for AML_M6 when AML_M6 is distinguished from all other AML subtypes,

10   and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, and/or 50 of Table 6.1, and/or

15   a higher expression a polynucleotide defined by any of the numbers 36, and/or 49 of Table 6.1

is indicative for AML_M0 when AML_M0 is distinguished from AML_M1,

and/or wherein

20   a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 6.2

is indicative for AML_M0 when AML_M0 is distinguished from

25   AML_M2,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 6.3, and/or

30   a higher expression of at least one polynucleotide defined by any of the numbers 9 of Table 6.3,

is indicative for AML_M0 when AML_M0 is distinguished from AML_M4,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 3, 5, 7, 9, 11, 12, 14, 18, 26, 32, 33, 34, 35, 36, 39, 40, 41, 42, 43, 44, 45, 47, 48, and/or 49, of Table 6.4, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 2, 4, 6, 8, 10, 13, 15, 16, 17, 19, 20, 21, 22, 23, 24, 25, 27, 28, 29, 30, 31, 37, 38, 46, and/or 50 of Table 6.4,

is indicative for AML_M0 when AML_M0 is distinguished from AML_M5a,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 6.5

is indicative for AML_M0 when AML_M0 is distinguished from AML_M5b

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 7, 8, 9, 10, 18, 26, 27, 28, 30, 32, 34, 35, 36, 37, 39, 46, 47, 48, and/or 49, of Table 6.6, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 11, 12, 13, 14, 15, 16, 17, 19, 20, 21, 22, 23, 24, 25, 29, 31, 33, 38, 40, 41, 42, 43, 44, 45, and/or 50 of Table 6.6

is indicative for AML_M0 when AML_M0 is distinguished from AML_M6,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 37, 40, 41, 42, 44, 45, 46, 47, 48, 49, and/or 50 of Table 6.7

a higher expression of at least one polynucleotide defined by any of the numbers 9, 24, 36, 38, 39, and/or 43, of Table 6.7

is indicative for AML_M1 when AML_M1 is distinguished from AML_M2,

5   and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 4, 5, 6, 7, 8, 9, 10, 11, 13, 15, 17, 18, 19, 21, 22, 24, 25, 26, 27, 28, 29, 30, 31, 32, 34, 35, 36, 37, 38, 40, 41, 42, 43, 44, 45, 47, 48, 49, and/or 50 of Table 6.8, and/or

10   a higher expression of at least one polynucleotide defined by any of the numbers 3, 12, 14, 16, 20, 23, 33, 39, and/or 46 of Table 6.8,

is indicative for AML_M1 when AML_M1 is distinguished from AML_M4,

and/or wherein

15   a lower expression of at least one polynucleotide defined by any of the numbers 23, 25, and/or 47, of Table 6.9, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 24, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40,

20   41, 42, 43, 44, 45, 46, 48, 49, and/or 50 of Table 6.9,

is indicative for AML_M1 when AML_M1 is distinguished from AML_M5a,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the

25   numbers 1, 2, 3, 4, 5, 7, 8, 9, 10, 11, 12, 13, 14, 15, 17, 18, 20, 22, 23, 24, 26, 28, 29, 31, 32, 33, 35, 38, 40, 41, 42, 45, 46, 48, 49, and/or 50 of Table 6.10, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 6, 16, 19, 21, 25, 27, 30, 34, 36, 37, 39, 43, 44, and/or 47 of

30   Table 6.10

is indicative for AML_M1 when AML_M1 is distinguished from AML_M5b,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 19, 22, 38, and/or 45, of Table 6.11, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 20, 21, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 39, 40, 41, 42, 43, 44, 46, 47, 48, 49, and/or 50 of Table 6.11

is indicative for AML_M1 when AML_M1 is distinguished from AML_M6,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 16, 17, 18, 20, 21, 22, 23, 24, 25, 26, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 43, 45, 46, 47, 49, and/or 50 of Table 6.12, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 14, 15, 19, 27, 40, 41, 42, 44, and/or 48 of table 6.12,

is indicative for AML_M2 when AML_M2 is distinguished from AML_M4,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 12 of Table 6.13, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 6.13

is indicative for AML_M2 when AML_M2 is distinguished from AML_M5a,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 14, 15, 16, 18, 19, 20, 21, 23, 24, 25, 26, 28, 32, 33, 34, 37, 38, 39, 40, 41, 42, 43, 44, 45, 47, 49, and/or 50 of Table 6.14, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 13, 17, 22, 27, 29, 30, 31, 35, 36, 46, and/or 48 of Table 6.14,

is indicative for AML_M2 when AML_M2 is distinguished from AML_M5b,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 26, 36, and/or 46, of Table 6.15, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 27, 28, 29, 30, 31, 32, 33, 34, 35, 37, 38, 39, 40, 41, 42, 43, 44, 45, 47, 48, 49, and/or 50 of Table 6.15

is indicative for AML_M2 when AML_M2 is distinguished from AML_M6,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 18, 21, 25, 28, 29, 36, 40, 43, and/or 46, of Table 6.16, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 19, 20, 22, 23, 24, 26, 27, 30, 31, 32, 33, 34, 35, 37, 38, 39, 41, 42, 44, 45, 47, 48, 49, and/or 50 of Table 6.16

is indicative for AML_M4 when AML_M4 is distinguished from AML_M5a,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 7, 9, 10, 12, 13, 15, 18, 19, 22, 25, 26, 28, 31, 32, 33, 37, 38, 40, 42, 47, and/or 50 of Table 6.17, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 5, 6, 8, 11, 14, 16, 17, 20, 21, 23, 24, 27, 29, 30, 34, 35, 36, 39, 41, 43, 44, 45, 46, 48, and/or 49 of Table 6.17,

is indicative for AML_M4 when AML_M4 is distinguished from AML_M5b,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 39, 40, 41, and/or 47 of Table 6.18, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 42, 43, 44, 45, 46, 48, 49, and/or 50 of Table 6.18,

is indicative for AML_M4 when AML_M4 is distinguished from AML_M6,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 2, 3, 4, 5, 6, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 23, 24, 26, 27, 28, 29, 31, 34, 35, 36, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 6.19, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 7, 22, 25, 30, 32, 33, and/or 37 of Table 6.19,

is indicative for AML_M5a when AML_M5a is distinguished from AML_M5b,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 15, 17, 18, 20, 23, 28, 29, 31, 37, 43, 44, 45, 46, and/or 48, of Table 6.20,

a higher expression of at least one polynucleotide defined by any of the numbers 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 16, 19, 21, 22, 24, 25, 26, 27, 30, 32, 33, 34, 35, 36, 38, 39, 40, 41, 42, 47, 49, and/or 50 of Table 6.20

is indicative for AML_M5a when AML_M5a is distinguished from AML_M6,

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 40, and/or 48, of Table 6.21, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 41, 42, 43, 44, 45, 46, 47, 49, and/or 50 of Table 6.21

is indicative for AML_M5b when AML_M5b is distinguished from AML_M6;

and/or wherein

a lower expression of at least one polynucleotide defined by any of the numbers 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 18, 19, 20, 21, 22, 23, 24, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, and/or 50 of Table 7, and/or

a higher expression of at least one polynucleotide defined by any of the numbers 16, 17, and/or 25, of Table 7

is indicative for AML_M3 when AML_M3 is distinguished from

AML_M3v.

2. The method according to claim 1 wherein the polynucleotide is labelled.

3. The method according to claim 1 or 2, wherein the label is a luminescent, preferably a fluorescent label, an enzymatic or a radioactive label.

4. The method according at least one of the claims 1-3, wherein the expression level of at least two, preferably of at least ten, more preferably of at least 25, most preferably of 50 of the markers of at least one of the Tables 1-7 is determined.

5. The method according to at least one of the claims 1-4, wherein the expression level of markers expressed lower in a first subtype than in at least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold lower, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold lower in the first subtype.

6. The method according to at least one of the claims 1-4, wherein the expression level of markers expressed higher in a first subtype than in at

least one second subtype, which differs from the first subtype, is at least 5 %, 10% or 20%, more preferred at least 50% or may even be 75% or 100%, i.e. 2-fold higher, preferably at least 10-fold, more preferably at least 50-fold, and most preferably at least 100-fold higher in the first subtype.

7.   The method according to at least one of the claims 1-6, wherein the sample is from an individual having AML.

8.   The method according to at least one of the claims 1-7, wherein at least one polynucleotide is in the form of a transcribed polynucleotide, or a portion thereof.

9.   The method according to claim 8, wherein the transcribed polynucleotide is a mRNA or a cDNA.

10.   The method according to claim 8 or 9, wherein the determining of the expression level comprises hybridizing the transcribed polynucleotide to a complementary polynucleotide, or a portion thereof, under stringent hybridization conditions.

11.   The method according to at least one of the claims 1-7, wherein at least one polynucleotide is in the form of a polypeptide, or a portion thereof.

12.   The method according to at least one of the claims 8, 9 or 12, wherein the determining of the expression level comprises contacting the polynucleotide or the polypeptide with a compound specifically binding to the polynucleotide or the polypeptide.

13.   The method according to claim 12, wherein the compound is an antibody, or a fragment thereof.

14. The method according to at least one of the claims 1-13, wherein the method is carried out on an array.

5 15. The method according to at least one of the claims 1-14, wherein the method is carried out in a robotics system.

16. The method according to at least one of the claims 1-15, wherein the method is carried out using microfluidics.

10

17. Use of at least one marker as defined in at least one of the claims 1-3 for the manufacturing of a diagnostic for distinguishing WHO classified AML subtypes AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a,

15 AML_M5b, AML_M6, AML_t(15;17)/M3 and/or AML_t(15;17)/M3v.

18. The use according to claim 17 for distinguishing AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a, AML_M5b, AML_M6,

20 AML_t(15;17)/M3 and/or AML_t(15;17)/M3v in an individual having AML.

19. A diagnostic kit containing at least one marker as defined in at least one of the claims 1-3 for distinguishing WHO classified AML subtypes

25 AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a, AML_M5b, AML_M6, AML_t(15;17)/M3 and/or AML_t(15;17)/M3v, in combination with suitable auxiliaries.

20. The diagnostic kit according to claim 19, wherein the kit contains a reference for the AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a, AML_M5b, AML_M6, AML_t(15;17)/M3 and/or AML_t(15;17)/M3v subtype.

21. The diagnostic kit according to claim 20, wherein the reference is a sample or a data bank.

22. An apparatus for distinguishing AML subtype AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a, AML_M5b, AML_M6, AML_t(15;17)/M3 and/or AML_t(15;17)/M3v in a sample containing a reference data bank.

23. The apparatus according to claim 22, wherein the reference data bank is obtainable by comprising
   (a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, 3, 4, 5, 6 and/or 7, and
   (b) classifying the gene expression profile by means of a machine learning algorithm.

24. The apparatus according to claim 23, wherein the machine learning algorithm is selected from the group consisting of Weighted Voting, K-Nearest Neighbors, Decision Tree Induction, Support Vector Machines, and Feed-Forward Neural Networks, preferably Support Vector Machines.

25. The apparatus according to at least one of the claims 22-24, wherein the apparatus contains a control panel and/or a monitor.

26. A reference data bank for distinguishing WHO classified AML subtype AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a, AML_M5b, AML_M6, AML_t(15;17)/M3 and/or AML_t(15;17)/M3v obtainable by comprising

    (a) compiling a gene expression profile of a patient sample by determining the expression level of at least one marker selected from the markers identifiable by their Affymetrix Identification Numbers (affy id) as defined in Tables 1, 2, 3, 4, 5, 6 and/or 7, and

    (b) classifying the gene expression profile by means of a machine learning algorithm.

27. The reference data bank according to claim 26, wherein the reference data bank is backed up and/or contained in a computational memory chip.

(54) Title: METHOD FOR DISTINGUISHING WHO CLASSIFIED AML SUBTYPES

(57) Abstract: Disclosed is a method for distinguishing WHO classified AML subtypes AML_MLL, t(15;17), t(8;21), inv(16),
11q23, de novo_AML, s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a, AML_M5b, AML_M6,
AML_t(15;17)/M3 and/or AML_t(15;17)/M3v in a sample by determining the expression level of markers, as well as a diagnostic
kit and an apparatus containing the markers.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP2004/012471

A. CLASSIFICATION OF SUBJECT MATTER
IPC 7   G01N33/574   C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
IPC 7   G01N   C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal, BIOSIS, WPI Data, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category °	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	WO 03/039443 A (DEUTSCHES KREBSFORSCH ;HAFERLACH TORSTEN (DE); EILS ROLAND (DE); K) 15 May 2003 (2003-05-15) the whole document in particular Examples 4, 6 and 7 ----- -/--	1-27

[X] Further documents are listed in the continuation of box C.

[X] Patent family members are listed in annex.

° Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search	Date of mailing of the international search report
3 March 2005	0 9. 06. 2005

Name and mailing address of the ISA	Authorized officer
European Patent Office, P.B. 5818 Patentlaan 2 NL - 2280 HV Rijswijk Tel. (+31-70) 340-2040, Tx. 31 651 epo nl, Fax: (+31-70) 340-3016	Thumb, W

Form PCT/ISA/210 (second sheet) (January 2004)

page 1 of 5

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category°	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	SCHOCH CLAUDIA ET AL: "Acute myeloid leukemias with reciprocal rearrangements can be distinguished by specific gene expression profiles" PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF USA, NATIONAL ACADEMY OF SCIENCE. WASHINGTON, US, vol. 99, no. 15, 23 July 2002 (2002-07-23), pages 10008-10013, XP002215484 ISSN: 0027-8424 the whole document in particular tables 1 and 2 -----	1-27
Y	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), SCHMITZ NICOLE ET AL: "Gene Expression Profiling in Acute Promyelocytic Leukemia (APL) with t(15;17) - Microarray Analyses and Validation of Important Genes Using Real Time PCR." XP002269979 Database accession no. PREV200300335808 abstract & BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 1208, 44th Annual Meeting of the American Society of Hematology;Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971 -----	1-27
Y	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), HAFERLACH TORSTEN ET AL: "Genetic Profiling in Acute Monoblastic Versus Acute Monocytic Leukemia: A Gene Expression Study on 22 Patients." XP002269980 Database accession no. PREV200300357649 abstract & BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 734, 44th Annual Meeting of the American Society of Hematology;Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971 ----- -/--	1-27

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category°	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), HAFERLACH TORSTEN ET AL: "Gene Expression Profiling Is Able To Reproduce Different Phenotypes in AML as Defined by the FAB Classification." XP002269981 Database accession no. PREV200300357598 abstract & BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 731, 44th Annual Meeting of the American Society of Hematology;Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971 -----	1-27
Y	SCHOCH CLAUDIA ET AL: "Acute myeloid leukemia with recurring chromosome abnormalities as defined by the WHO-classification: Incidence of subgroups, additional genetic abnormalities, FAB subtypes and age distribution in an unselected series of 1,897 patients with acute myeloid leukemia." HAEMATOLOGICA, vol. 88, no. 3, March 2003 (2003-03), pages 351-353, XP009025472 ISSN: 0390-6078 (ISSN print) the whole document -----	1-27
Y	KOHLMANN A ET AL: "MOLECULAR CHARACTERIZATION OF ACUTE LEUKEMIAS BY USE OF MICROARRAY TECHNOLOGY" GENES, CHROMOSOMES & CANCER, XX, XX, vol. 37, no. 4, August 2003 (2003-08), pages 396-405, XP008025253 the whole document in particular table 2 -----	1-27

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C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category°	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2001 (2001-11-16), SCHOCH CLAUDIA ET AL: "Specific abnormalities on the genomic level result in a distinct gene expression pattern detected by oligonucleotide microarrays: An analysis of 25 patients with AML M2/t(8;21), AML M3/M3v/t(15;17), and AML M4eo/inv(16)" XP002269491 Database accession no. PREV200200129822 abstract & BLOOD, vol. 98, no. 11 Part 1, 16 November 2001 (2001-11-16), pages 92a-93a, 43rd Annual Meeting of the American Society of Hematology, Part 1;Orlando, Florida, USA; December 07-11, 2001 ISSN: 0006-4971 -----	1-27
Y	EP 1 043 676 A (WHITEHEAD BIOMEDICAL INST) 11 October 2000 (2000-10-11) the whole document -----	1-27
Y	GOLUB T R ET AL: "Molecular classification of cancer: Class discovery and class prediction by gene expression monitoring" SCIENCE, AMERICAN ASSOCIATION FOR THE ADVANCEMENT OF SCIENCE,, US, vol. 286, no. 5439, 15 October 1999 (1999-10-15), pages 531-537, XP002207658 ISSN: 0036-8075 cited in the application the whole document -----	1-27
Y	DUGAS M ET AL: "A comprehensive leukemia database: integration of cytogenetics, molecular genetics and microarray data with clinical information, cytomorphology and immunophenotyping" LEUKEMIA, MACMILLAN PRESS LTD, US, vol. 15, no. 12, December 2001 (2001-12), pages 1805-1810, XP002263731 ISSN: 0887-6924 the whole document -----	1-27

-/--

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category°	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	DUGAS MARTIN ET AL: "Impact of integrating clinical and genetic information." IN SILICO BIOLOGY, vol. 2, no. 3, 2002, pages 383-391, XP001179418 ISSN: 1386-6338 (ISSN print) the whole document	1-27
A	US 2003/138793 A1 (SU ANDREW I ET AL) 24 July 2003 (2003-07-24) paragraphs [0014], [0015]	1-27
A	RODRIGUEZ S ET AL: "Expression profile of genes from 12p in testicular germ cell tumors of adolescents and adults associated with i(12p) and amplification at 12p11.2-p12.1." ONCOGENE, vol. 22, no. 12, 27 March 2003 (2003-03-27), pages 1880-1891, XP002269982 ISSN: 0950-9232 (ISSN print) abstract	1-27
A	ALIZADEH A ET AL: "THE LYMPHOCHIP: A SPECIALIZED CDNA MICROARRAY FOR THE GENOMIC-SCALE ANALYSIS OF GENE EXPRESSION IN NORMAL AND MALIGNANT LYMPHOCYTES" COLD SPRING HARBOR SYMPOSIA ON QUANTITATIVE BIOLOGY, BIOLOGICAL LABORATORY, COLD SPRING HARBOR, NY, US, vol. 64, no. 1, 1999, pages 71-78, XP001099007 ISSN: 0091-7451 the whole document	1-27
A	DATABASE BIOSIS [Online] BIOSCIENCES INFORMATION SERVICE, PHILADELPHIA, PA, US; 16 November 2002 (2002-11-16), KOHLMANN ALEXANDER ET AL: "A Simplified and Partially Automated Target Preparation Method for Gene Expression Profiling." XP002269495 Database accession no. PREV200300367771 abstract & BLOOD, vol. 100, no. 11, 16 November 2002 (2002-11-16), page Abstract No. 4287, 44th Annual Meeting of the American Society of Hematology;Philadelphia, PA, USA; December 06-10, 2002 ISSN: 0006-4971	1-27

Box II Observations where certain claims were found unsearchable (Continuation of item 2 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. [X] Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:

Article 52 (2)(d) EPC - Presentation of information

The claims were only searched with regards to the underlying method of generating a reference data base for distinguishing leukemia subtypes.

2. [ ] Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:

3. [ ] Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box III Observations where unity of invention is lacking (Continuation of item 3 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. [ ] As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.

2. [ ] As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.

3. [ ] As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:

4. [X] No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-27 (partially)

Remark on Protest   [ ] The additional search fees were accompanied by the applicant's protest.

[ ] No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM   PCT/ISA/ 210

This International Searching Authority found multiple (groups of)
inventions in this international application, as follows:

1. claims: 1-27 (partially)

    A method for distinguishing WHO-classified AML subtypes
    AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML,
    s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a,
    AML_M5b, AML_M6, AML_t(15;17)/M3 and/or AML_t(15;17)/M3v,
    the method comprising determining the expression level of
    the marker BCAT1. Use of said marker for the manufacture of
    a diagnostic. A diagnostic kit containing said marker and an
    apparatus comprising a reference data bank, wherein the
    reference data bank is obtainable by determining the
    expression level of BCAT1.
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2. claims: 1-27 (all partially)

    Inventions 2-2450
    Methods for distinguishing WHO-classified AML subtypes
    AML_MLL, t(15;17), t(8;21), inv(16), 11q23, de novo_AML,
    s_AML, t_AML, AML_M0, AML_M1, AML_M2, AML_M4, AML_M5a,
    AML_M5b, AML_M6, AML_t(15;17)/M3 and/or AML_t(15;17)/M3v,
    and methods for distinguishing specific subtypes against all
    other AML subtypes and against each other, the method
    comprising determining individually the expression level of
    the markers listed in tables 1.1, positions 2-50,and in
    tables 2-7. Use of said markers for the manufacture of
    diagnostics. Diagnostic kits containing said markers and
    apparatus' comprising a reference data bank, wherein the
    reference data bank is obtainable by determining the
    expression levels of said markers.

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